

## SUMMARIES

printed

02 ; Search time 5999

16639.355 Million c

.....tttttttttt

residues

Parameters: 5777422

redicted by chance t

Description
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AR214341 Sequence
U91994 Sus scrofa
AB051013 Felis cat
BC010140 Homo sapi
M63121 Human tumor
M33294 Human tumor
AA3873 Sequence 1
A78738 Sequence 7
AR041076 Sequence
164751 Sequence 1
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AX049713 Sequence
AX558239 Sequence
M58286 Homo sapien
AR096630 Sequence
AX531005 Sequence
AX57013 H. sapiens T
AI19907 Synthetic n
A21552 TMR alpha g
I43805 Sequence 24
A20255 5SKD recept
AX056611 Homo sapi
M602275 Human tumor
A29098 Synthetic D
AR302865 Sequence
AX330421 Sequence
AX401925 Sequence
M63122 Rat tumor n
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AR329979 Rattus no
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AR329976 Rattus no
AR329977 Rattus no
L26349 Mus musculu
M57796 Mus muscu
A29103 H. sapiens m
M59377 Murine tumo
M60466 Mouse tumor
AY52328 Murine mRNA
BC004539 Mus muscu
BC052675 Mus muscu
AR214342 Sequence
I26928 Sequence 2

ar MAM 21-JAN-2000  
NF-RT) mRNA, complete  
ata; Euteleostomi;  
a; Pecora; Bovoidae;

FEATURES	source	1..2440
JOURNAL	Conting and sequencing of cDNA encoding bovine tumor necrosis factor (TNF)-receptor 1	
MEDLINE	Vec. Immunol. Immunopathol. 61 (2-4), 379-385 (1998)	
PUBMED	98273505	
REFERENCE	2 (bases 1 to 2440)	
AUTHORS	Lee, B.-K., Talvor, M.J. and Kehrl, M.E.	
TITLE	Direct Submission	
JOURNAL	Submitted (26-FEB-1997) Metabolic Disease and Immunology, National Animal Disease Center, 2300 Dayton Ave., Ames, IA 50010, USA	
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ORIGIN		
Query Match	100.0%; Score 2440; DB 4; Length 2440;	
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DB	1 TTTTATTTTTTTTTTTCTTTTGGGGGGAAGGGGTGACCCCTTCTCCACC	60
QY	TCCTCTCAGCTCAAGTTTCTCGAGAGCTCTCGGGCTCTGGGCGGAGGGCTGGCTTC	120
DB	61 TCCTCTCAGCTCAAGTTTCTCGAGAGCTCTCGGGCTCTGGGCGGAGGGCTGGCTTC	120
QY	121 GGGTTTGAAGTCTTCGGATTGGGCTGTGTCCCGCCCACTCTCAACCTTCACTCCC	180
DB	121 GGGTTTGAAGTCTTCGGATTGGGCTGTGTCCCGCCCACTCTCAACCTTCACTCCC	180
QY	181 GACCGAGGCGCGGGCTCTCACTGGGAGACCGGAGACCGTGTGTCTCACTGTCCGG	240
DB	181 GACCGAGGCGCGGGCTCTCACTGGGAGACCGGAGACCGTGTGTCTCACTGTCCGG	240
QY	241 GCCGCACTGCGCCAGCCTGATGGGGGATTGAGAGGCGCAGAGCTGGCGGAGATGGGCC	300
DB	241 GCCGCACTGCGCCAGCCTGATGGGGGATTGAGAGGCGCAGAGCTGGCGGAGATGGGCC	300
QY	301 TCCCAACCGTGTCTGGCTGCTGCTGCCACTGTGTCTTCAGCTCTGTGGCAGATGTGT	360
DB	301 TCCCAACCGTGTCTGGCTGCTGCTGCCACTGTGTCTTCAGCTCTGTGGCAGATGTGT	360
QY	361 ACCCGGAGGGGTTCAAGGGCTGTGATCCCTACCCCGGGGACCTGGAGAGAGAGAGTCC	420
DB	361 ACCCGGAGGGGTTCAAGGGCTGTGATCCCTACCCCGGGGACCTGGAGAGAGAGAGTCC	420
QY	421 CTTGTCCCAAGAGAAATATTAACCAACCGGCAAAATAGACCATTTGTGCAACAAAGTCC	480
DB	421 CTTGTCCCAAGAGAAATATTAACCAACCGGCAAAATAGACCATTTGTGCAACAAAGTCC	480

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QY	601	CGAGGTGCCGGGACGAAATGTTCCAGGTGGGAAATTTGCTGTGTGTAGTGGACCCGGAC	660
Db	601	CGAGGTGCCGGGACGAAATGTTCCAGGTGGGAAATTTGCTGTGTGTAGTGGACCCGGAC	660
QY	661	CTGTGTGCGGCTGCAGGAAGAACCGAGTAATCTGGGGTAAACTGAGCTTCCGGT	720
Db	661	CTGTGTGCGGCTGCAGGAAGAACCGAGTAATCTGGGGTAAACTGAGCTTCCGGT	720
QY	721	GTTCTGAATGACAGGCTCTGTCTCCAAATGGCACAAGTAATATCCCTCCGACGAGACACAG	780
Db	721	GTTCTGAATGACAGGCTCTGTCTCCAAATGGCACAAGTAATATCCCTCCGACGAGACACAG	780
QY	781	ACACCATCTGCCACTGSCATATGAGCTTCTTTCTTAAAGGCGCCAAAGTCATCTGTCTG	840
Db	781	ACACCATCTGCCACTGSCATATGAGCTTCTTTCTTAAAGGCGCCAAAGTCATCTGTCTG	840
QY	841	ATGATTGTAAAGAACAGGATGTGCGAAGATTATGTCCAACTCCGACTTTCACCTGTGTAAG	900
Db	841	ATGATTGTAAAGAACAGGATGTGCGAAGATTATGTCCAACTCCGACTTTCACCTGTGTAAG	900
QY	901	ACTCTCAGAGACCCAGGACCTACAGTACATTAACCCCTGTGTAATGTCTTCCGGCTTTGCC	960
Db	901	ACTCTCAGAGACCCAGGACCTACAGTACATTAACCCCTGTGTAATGTCTTCCGGCTTTGCC	960
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Db	961	TGGACATCTTGCCTCTGTGTGCTTTAGCATGTGCTTACAGCGGTGGAAGCCCAAGCTCT	1020
QY	1021	ACTCCATCATTTGGCGGGAGTGCACCTCTGTGTAAAGAGGGGAGCCAGAACTTCTGTGCTC	1080
Db	1021	ACTCCATCATTTGGCGGGAGTGCACCTCTGTGTAAAGAGGGGAGCCAGAACTTCTGTGCTC	1080
QY	1081	CGGCCCCAGGCTTCAACCCCAACAACATCTGTGAGCTGCCACCCCAAGTTTCAAGTC	1140
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QY	1141	CTGTCTGCATTTCCCCCTTACATCTCTCTGTGACCGGTCCAACTTTGGAGCGCTCGCATCTC	1200
Db	1141	CTGTCTGCATTTCCCCCTTACATCTCTCTGTGACCGGTCCAACTTTGGAGCGCTCGCATCTC	1200
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Db	1201	CCTCCAGGAGACGAGGCCCGGCCCATCTTAAAGGCTGGGCCCATCTCCCGGGGCTCCGCG	1260
QY	1261	CCTCCAGGAGACGAGGCCCGGCCCATCTTAAAGGCTGGGCCCATCTCCCGGGGCTCCGCG	1320
Db	1261	CCTCCAGGAGACGAGGCCCGGCCCATCTTAAAGGCTGGGCCCATCTCCCGGGGCTCCGCG	1320
QY	1321	CTTCCGGGCTTCCACCACTCTGACACCCCAAGTTCAAGAGTGGGAAGCCAGCCGCCCAAGC	1380
Db	1321	CTTCCGGGCTTCCACCACTCTGACACCCCAAGTTCAAGAGTGGGAAGCCAGCCGCCCAAGC	1380
QY	1381	CCCCCGATCAAGCTGTGCGGATGTCCAGACCCCGGACCTGTGATGCGGCTGTGGAAGGGCGTGC	1440
Db	1381	CCCCCGATCAAGCTGTGCGGATGTCCAGACCCCGGACCTGTGATGCGGCTGTGGAAGGGCGTGC	1440
QY	1441	CCCCGTGTGCGCTGTGAAAGAGTTGGTGTGGGGGCTGTGGACTGAGCGGACGAGATCTGAGC	1500
Db	1441	CCCCGTGTGCGCTGTGAAAGAGTTGGTGTGGGGGCTGTGGACTGAGCGGACGAGATCTGAGC	1500
QY	1501	GGCTGTGAGCTGTGAAAGAGGGGCGCCACTGTGCGGAGGCGGACGAGTACAGATGTGTGCGGGCT	1560
Db	1501	GGCTGTGAGCTGTGAAAGAGGGGCGCCACTGTGCGGAGGCGGACGAGTACAGATGTGTGCGGGCT	1560



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Db      901 ACTCTAGAGACCCAGGACCTAAGTACTTACCCCTGGATTTGCTTCCGCTTTGGC 960
Qy      961 TGGCATCTTCTGCTCTGTGTCTTATGATGTGCTTACCAAGCGGTGAAGCCCAAGCTCT 1020
Db      961 TGGCATCTTCTGCTCTGTGTCTTATGATGTGCTTACCAAGCGGTGAAGCCCAAGCTCT 1020
Qy      1021 ACTCATCATTTTTCGGGAGTGCATCTGGTAAAGAGGGGGAGGCAAGAACTCTGTGTCC 1080
Db      1021 ACTCATCATTTTTCGGGAGTGCATCTGGTAAAGAGGGGGAGGCAAGAACTCTGTGTCC 1080
Qy      1081 CGGCCCCAGGCTTCAAGCCCAACCAACCATCTGTTCAGCTTCACCCCAAGTTCCAGTC 1140
Db      1081 CGGCCCCAGGCTTCAAGCCCAACCAACCATCTGTTCAGCTTCACCCCAAGTTCCAGTC 1140
Qy      1141 CTGTCTCATTTCCCTTATCATCTCTGTGACCGGTCCAACTTCGGAGCCGTGCAATCTC 1200
Db      1141 CTGTCTCATTTCCCTTATCATCTCTGTGACCGGTCCAACTTCGGAGCCGTGCAATCTC 1200
Qy      1201 CCTCCAGCAGACGGCCCGCCCATCTAAAGGCTGGCCCATCTCCCGGGGCTCCGGG 1260
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Qy      1261 CCTCCACCACTCTGTATACCCCGGGGCTCCGGGCTTCCACCACTCTGTATACCCCGGGG 1320
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Qy      1861 GATCTGGAGAGGACCTGATCTGTGTACTACTAGTACTAGTCTTTCTCAGCTGCC 1920
Db      1861 GATCTGGAGAGGACCTGATCTGTGTACTACTAGTACTAGTCTTTCTCAGCTGCC 1920
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Qy      1981 TGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
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Db      1981 TGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
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Db      2041 CCAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100
Qy      2101 GAGAACTAGCAAGGCGACTTGGGGAACCTTACGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
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Qy      2161 ATAAAGCATCTTTTGTATCATCTGTGACATCATCATCATCATCATCATCATCATCATCAT 2220
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Qy      2281 TGGGGCTTCCCAAGGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
Db      2281 TGGGGCTTCCCAAGGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
Qy      2341 CTTTGCAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Db      2341 CTTTGCAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
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**RESULT 3**  
**LOCUS** SSU19994  
**DEFINITION** Sus scrofa p55 TNF receptor mRNA, complete cds.  
**VERSION** U19994  
**KEYWORDS** U19994.1 GI:1141752  
**SOURCE**  
**ORGANISM** Sus scrofa (pig)  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
**AUTHORS** Suter, B. and Pauli, U.  
**TITLE** Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
**JOURNAL** Gene 163 (2), 263-266 (1995)  
**MEDLINE** 96011645  
**PUBMED** 7590278  
**REFERENCE** 2 (bases 1 to 2004)  
**AUTHORS** Pauli, U. H.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (19-JAN-1995) Urs H. Pauli, Veterinary Virology, University of Bern, Laenggasse-Str. 122, Bern CH-3012, Switzerland  
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OY 2278 AAATGGGCGCTCCCAAGGAGCT 2300
DB 1981 CAATGGGCGCTTCAGCTGAGCT 2003

RESULT 4
AB051103
LOCUS
DEFINITION
AB051103 2171 bp mRNA linear MAM 19-MAR-2002
Felis catus TNFR I mRNA for tumor necrosis factor type I, complete
cDNA
ACCESSION
AB051103
VERSION
AB051103.1 GI:14041808
KEYWORDS
Felis catus (cat)
SOURCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
1 Mizuno, T., Goto, Y., Baba, K., Masuda, K., Ohno, K. and Teujimoto, H.
TNF-alpha-induced cell death in feline immunodeficiency
virus-infected cells is mediated by the caspase cascade.
Virology 287 (2), 446-455 (2001)
JOURNAL
21425483
PUBMED
11531421
2 (bases 1 to 2171)
Mizuno, T.
REFERENCE
Submitted (14-NOV-2000) Takuya Mizuno, The University of Tokyo,
Department of Veterinary Internal Medicine, Yayoi 1-1-1, Bunkyo-ku,
Tokyo 113-8657, Japan (E-mail: ta7715@mail.ecc.u-tokyo.ac.jp,
Tel:81-3-5841-8004, Fax:81-3-5841-8178)
FEATURES
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Matches 1424; Conservative 0; Mismatches 495; Indels 145; Gaps 12;
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DB 147 GCGGCGACCTGCGCCAGCCCTGATGAGGAGATTGAGAGGCAACAGCTGGCGGACATGGGCC 206
OY 301 TCCCGACCGTGCCTGCTGCTGCTGCACTGTGCTTCCAGCTCTGTTGGCAGATGT 360
DB 207 TCCCGACCGTGCCTGCTGCTGCTGCACTGTGCTTCCAGCTCTGTTGGCAGATGT 266
OY 361 ACCCGCAGGGGTTTCAGGGGCTGTGCTTCACTCCCGGGGACCTTGAGAGAGAGATGC 420
DB 267 ACCCATTAAGGGTACTGAGCTGGTCCCTCACCTCAGGAGACCGGAGAGAGAGATATTC 326
OY 421 CCGTCCCGCAAGAAATATTAACAACCGCAAAATAGCAACATTTGCTGCAACCAAGTCC 480

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DB 327 CATGCCCCCAAGAAATATTAATTCACCTTCAAGATTAATTCATTTGCTGTAAGAAATGCC 386
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DB 507 CCAATATGCGAAAGAAATGTATACAGGTGAGATATCTCTTGCACAGTGTACCGGAGCA 566
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DB 627 GCTTAACCTGAGGCTGTGTCTCAACGCGACGTTGCAAGTCTCTGCAAGGAGACACAGA 686
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OY 841 ATGATTTGAG--AACAGAGATGCGAGAAATATGTCACACCCGACTTCAACTGTA 897
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OY 1318 GCGCTCCGCGCTTCAACCTCTGTGACCCCAAGTTCAAGAGTGGAGAGCAGCGGCCCA 1377
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OY 1438 TGCCTCCGTCGCGCTGAGAGAGATGAGTGGCGGCTGAGACTGAGAGCAGCAGATCG 1497
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OY 1498 AGGCGCTGAGCTGAGAGAGCGGCGCACTTGGCGAGGCGCAGTACAGACTCTGGCGG 1557

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Db      1389 CTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1448
Qy      1618 GGGAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1677
Db      1449 GTGACATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1508
Qy      1678 GCTTGGGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1737
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REMARK
COMMENT
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
nisc_mgcembgrl.nih.gov
Contact:
Shevchenko, Y., Weetebdy, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, O.L., Mastaglio, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stancirpop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAL Plate: 27 Row: m Column: 22
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 339755.
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Best Local Similarity 69.8%; Pred. No. 6.7e-120;
Matches 1176; Conservative 0; Mismatches 413; Indels 96; Gaps 9;
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Qy 125 TTGAGGCTCTCGGATTTGGGCTGTC---TCCCGCGCGGCGGCGGCGGCTCCCGG 181
Db 69 TCAAGATCTACTGGAGCAGGCGCGGATCTTATGCGCGAGCTCAACCTCACTGATC 128
Qy 182 ACCGAGGCGGCGGCTCACTGCGCATACGCGAGACGCTTCTGCTGCTGCTGCGCGG 241
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Qy 242 CCGGCACTGCGCC-AGCCCTGATGCGGCGGATTTGAGAGGCGGCGGCGGCGGCGGCGG 300
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 LOCUS  
 DEFINITION Homo sapiens, tumor necrosis factor receptor superfamily, member  
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 ACCESSION BC010140.1 GI:14603367  
 VERSION BC010140  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 2194)  
 Strausberg, R.  
 Direct Submission  
 Submitted (02-JUL-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

[illegible]

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OY	1420	ACGCGGTGTGTGAGAGCGGCGTGCCTTCGCGCTGGAGAGATTGATGTCGCGCGACTGGAGAC	1479
Db	1319	ACGCGGTGTGTGAGAACGTGTGCCCTTCGTGTGGCTGGAGGAAATTGTGTGCGGCGCTTAGGGC	1378
OY	1480	TGAGCCGAGACACGACATCGAGCGGCTTGGAGCTTGGAGAACGGGCGCCACCTGCGCGAGCGCC	1539
Db	1379	TGAGCCGACACACGAAATGATCGCTGTGAGCTGCGAAGACGGGCGCTGCTCGCGCAGCGCG	1438
OY	1540	AGTACAGCATGCTGGCGGCGCTGGCGGGGGGACACCGCGCCCGCGAGGCCACCGTTGGAGC	1599
Db	1439	AATTACAGCATGTGTGGCACTTGAAGGGGGGACACCGCGCGCGAGGCCACCGTTGGAGC	1498
OY	1600	TGCTGGGCGCGGTGTCTCAGGAGACATTGACCTGTGCTGAGTTCTCTGGAAACATAGAGAGG	1659
Db	1499	TGCTGGGACGGGTGTCTCGGGACATTTGACCTGTCTGGGCTCCCTGGAGGACATGTAGGAGG	1558
OY	1660	CGCTGGGTGGCGCCCGCGCTTGCGGTCCGAGCCCGCGCTTCTTGTGTGAAGCCCGCGCC	1719
Db	1559	CGCTTGTGGGCGCCCGCGCGCTCCCGCGCGCCGACAGTCTTCTCAGATGAGGCTGCGGCC	1618
OY	1720	CTCGG 1724	
Db	1619	CTGGG 1623	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
HUMTNTRC	Human tumor necrosis factor receptor (TNF receptor)	M63121	M75861	tumor necrosis factor receptor.	Homo sapiens (human)	Homo sapiens
LOCUS	2112 bp mRNA linear	M63121.1	G1:339755		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE		1 (bases 1 to 2112)			Hämmler, A., Mauver-Fogay, I., Kronke, M., Scheurich, P., Pfizenmayer, K., Lantzi, M., Olsson, I., Hauptmann, R., Strätowa, C. and Adolf, G.R.	
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
COMMENT						
FEATURES						
source						
gene						
CDS						

sig\_peptide 207..293  
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BASE COUNT 435 a 632 c 589 g 456 t  
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Query Match 30.2%; Score 735.8; DB 9; Length 2112;  
Best Local Similarity 69.9%; Pred. No. 8.9e-119;  
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Db 71 CCACTTCAACCTTCACCTCCCGACCCGAGGACCTTGGAGCTCTGAGACAGACGAGTC 130
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Db 250 TCTTGAGACTGTGGTGGGAATATATACCTCAGGGGTTATTGAGCTGTCTCTCACCTAG 309
Oy 397 GGGACCTGGAAGAAGAGAGTCCCTGCTCCCAAGAAATATATACACCCGCAAAATA 456
Db 310 GGGACGAGGAAGAAGAGATGTGTGTCTCCCAAGAAATATATACACCTCAAAATA 369
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## RESULT 7

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LOCUS Human tumor necrosis factor receptor mRNA, complete cds.  
DEFINITION  
ACCESSION M33294  
VERSION M33294.1 GI:339744  
KEYWORDS cell surface receptor; tumor necrosis factor receptor.  
SOURCE  
ORGANISM Homo sapiens (human)

REFERENCE  
1 (bases 1 to 2087)  
Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,  
Gatanaga,T., Granger,G.A., Lenz,R., Raab,H., Kohl,W.J. and  
Goeddel,D.V.  
Molecular cloning and expression of a receptor for human tumor  
necrosis factor

JOURNAL  
Cell 61 (2), 361-370 (1990)  
MEDLINE  
2158653

TITLE  
JOURNAL  
MEDLINE  
PUBMED

COMMENT Original source text: Human placenta, cDNA to mRNA.  
 Draft entry and computer-readable sequence for [1] kindly submitted  
 by T. Schall, 26-MAR-1990.

FEATURES  
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ORIGIN

Query Match 29.9%; Score 728.6; DB 9; Length 2087;  
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 QY 327 CCACTGTGTCTTCCAGCTCTGTGGCAAGTGTGTAACCCCGAGGGGTTCAAGGGCTGTG 386  
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RESULT 8  
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 LOCUS  
 DEFINITION Sequence 1 from Patent EP0657536.

ACCESSION A43873  
 VERSION A43873.1 GI:2299022  
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 SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE 1 (bases 1 to 2175)  
 AUTHORS Wallach, D., Brackebusch, C., Varfolomeev, E. and Balkin, M.  
 TITLE Proteases capable of shedding the soluble TNF-receptor and TNF-R derived peptides and antibodies against the proteases inhibiting the shedding  
 JOURNAL Patent: EP 0657536-A 1 14-JUN-1995;  
 YEDA RES & DEV (IL)  
 COMMENT Other publication ZA 9407962 951121  
 Other publication JP 7194376 950801  
 Other publication AU 7574294 950504  
 Other publication CA 2133872 950413.  
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 BASE COUNT 474 a 641 c 604 g 456 t  
 ORIGIN  
 Query Match 29.8%; Score 727; DB 6; Length 2175;  
 Best Local Similarity 69.6%; Pred. No. 3,1e-117;  
 Matches 112; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

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Query 9  
LOCUS A78738 2175 bp DNA linear PAT 19-OCT-1999  
DEFINITION Sequence 7 from Patent EP0568925.  
ACCESSION A78738  
VERSION A78738.1 GI:6090341  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 2175)  
AUTHORS Brakebush, C. and Wallach, D.  
TITLE TNF RECEPTOR ACTION MODULATION  
JOURNAL Patent: EP 0568925-A 7 10-NOV-1993;  
YEDA RES & DEV (IL)  
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Best Local Similarity 69.6%; Pred. No. 3.1e-117;  
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DEFINITION Sequence 1 from patent US 5811261.  
AR041076  
VERSION AR041076.1 GI:5961572  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2175)  
Wallach, D., Nopnar, Y., Kemper, O., Engelmann, H., Brakebusch, C. and  
Agerka, D.  
TITLE Expression of the recombinant tumor necrosis factor binding protein  
1 (TBF-1)  
JOURNAL Patent: US 5811261-A 1 22-SEP-1998;  
FEATURES  
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BASE COUNT 474 a 641 c 604 g 456 t  
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Query Match 29.8%; Score 727; DB 6; Length 2175;  
Best Local Similarity 69.6%; Pred. No. 3,1e-117;  
Matches 112; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

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DB 1600 CCGGCTGTGAGAGAGTGTGAG 1659  
QY 1746 C 1746  
DB 1660 C 1660

RESULT 11  
164751  
LOCUS 164751 2175 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 1 from patent US 5665859.  
 ACCESSION I64751  
 VERSION I64751.1 GI:2481645  
 KEYWORDS  
 SOURCE  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2175)  
 AUTHORS Wallach,D., Brakheusch,C., Varfolomeev,E. and Baklin,M.  
 TITLE Molecules influencing the shedding of the TNF receptor, their  
 preparation and their use  
 JOURNAL Patent: US 5665859-A 1 09-SEP-1997;  
 FEATURES Location/Qualifiers  
 source 1..2175  
 1..2175  
 ORGANISM="unknown"  
 BASE COUNT 474 a 641 c 604 g 456 t  
 ORIGIN  
 Query Match 29.8%; Score 727; DB 6; Length 2175;  
 Best Local Similarity 69.6%; Pred. No. 3.1e-117;  
 Matches 1129; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

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RESULT 12  
 LOCUS A26412 2111 bp DNA linear PAT 26-APR-1995  
 DEFINITION cDNA for (55KD TNF-BP) tumor necrosis factor binding protein from  
 patient EP0417563.  
 ACCESSION A26412  
 VERSION A26412.1 GI:904968  
 KEYWORDS  
 SOURCE Synthetic construct  
 ORGANISM Synthetic construct  
 artificial sequences.

REFERENCE 1 (bases 1 to 2111)  
 AUTHORS Brochhaus, M., Demic, Z., Gentz, R., Iesslaue, W., Loetscher, H. and  
 Schlagger, E. J.  
 TITLE TNF-binding proteins  
 JOURNAL Patent: EP 0417563-A 24 20-MAR-1991;  
 F. HOFMANN-LA ROCHE AG  
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REFERENCE  
1 Alvarado, C., Horne, D., Perez-da-Silva, S. and Vockley, J. G.  
Gene expression profiles in liver cancer  
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REFERENCE 1

## AUTHORS

Poulsen, H.S., Pedersen, N., Mortensen, S., Sorensen, S.B.,  
 Petersen, M.W., and Eisman, H.I.

## TITLE

Methods for identification of cancer cell surface molecules and  
 cancer specific promoters, and therapeutic uses thereof  
 Patent: WO 0300928-A 155 03-JAN-2003;

## JOURNAL

Odin Medical A/S (DK)

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 Loetscher, H., Pan, Y.C., Lahm, H.W., Gentz, R., Brockhaus, M.,  
 Tabuchi, H., and Lesslauer, W.  
 Molecular cloning and expression of the human 55 kd tumor necrosis  
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PA (USDA ) US SEC OF AGRIC.
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PI WPI; 2002-58816/63.
XX DR P-PsDB; AAE25816.
XX Novel nucleic acid molecule encoding bovine tumor necrosis factor
PT receptor-1 which is a potent inhibitor of tumor necrosis factor-alpha
PT useful for treating coliform mastitis or other inflammatory disease in
PT cattle
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XX Claim 1; Column 11-16; 16pp; English.
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XX The invention relates to an isolated nucleic acid encoding a polypeptide
XX that binds bovine tumor necrosis factor (TNF). The invention is useful
XX for expressing bovine TNF-R1 or soluble bovine TNF-R1 which is useful as
XX an inhibitor of TNF in cattle suffering from coliform mastitis or other
XX inflammatory disease. The nucleic acids and polypeptide or their
XX fragments are useful for treating mastitis. The present sequence is
XX bovine tumor necrosis factor receptor-1 (TNF-R1) cDNA.
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DB 181 GACCCGAGGCGCGGCTCCTCAGTGGGATTCGCGAGGACCGTGTCTGTCTGTCTGCGG 240
QY 241 GCGGCACTGCGCCAGCCCTGATGGGGGATTGAGAGGCCAGCTGGCCGACATGGGCG 300
DB 241 GCGGCACTGCGCCAGCCCTGATGGGGGATTGAGAGGCCAGCTGGCCGACATGGGCG 300
QY 301 TCCCCACGCTGCGGCTGTCTGTCTGCGACCTGTCTTCCAGCTCTGTGGAGATGTGT 360
DB 301 TCCCCACGCTGCGGCTGTCTGTCTGCGACCTGTCTTCCAGCTCTGTGGAGATGTGT 360
QY 361 ACCCGCAGGGGTTTCAAGGGCTGTCTCCTCACCCCGGGGACTGGAGAAAGAGAGAGTC 420
DB 361 ACCCGCAGGGGTTTCAAGGGCTGTCTCCTCACCCCGGGGACTGGAGAAAGAGAGAGTC 420
QY 421 CCTGTCTCCCAAGAAATATTAACAACCGCAAAATAGCAATTTGTCTGCAACCAATGCC 480
DB 421 CCTGTCTCCCAAGAAATATTAACAACCGCAAAATAGCAATTTGTCTGCAACCAATGCC 480
QY 481 ACMAAGGTAATCTATCTGTATGACTGTCTCGGGTTCAGGGGGAACAACGAGCTCAGGG 540
DB 481 ACMAAGGTAATCTATCTGTATGACTGTCTCGGGTTCAGGGGGAACAACGAGCTCAGGG 540
QY 541 TGTGTGCGCGCTGAGCACTACCTGCTTGGAGAACATCTCAGAGATGCTGAGCTGT 600
DB 541 TGTGTGCGCGCTGAGCACTACCTGCTTGGAGAACATCTCAGAGATGCTGAGCTGT 600
QY 601 CCAAGTGCAGGAGCAAAATGTTCCAGGTGAGATTTGCTGTGTAGTGAACCGGAGCA 660
DB 601 CCAAGTGCAGGAGCAAAATGTTCCAGGTGAGATTTGCTGTGTAGTGAACCGGAGCA 660
DB 601 CCAAGTGCAGGAGCAAAATGTTCCAGGTGAGATTTGCTGTGTAGTGAACCGGAGCA 660
QY 661 CTGTGTGCGCTGAGCAAGAAACAGTACCGGGGATATCTGGGGTGAACCTGGCTTCGG 720
DB 661 CTGTGTGCGCTGAGCAAGAAACAGTACCGGGGATATCTGGGGTGAACCTGGCTTCGG 720
QY 721 GTCTGAATGCAAGCTCTGTCTTCCCAATGAGCAAGTGAATATCCCTGCGAGAGAGACAG 780
DB 721 GTCTGAATGCAAGCTCTGTCTTCCCAATGAGCAAGTGAATATCCCTGCGAGAGAGACAG 780
QY 781 ACACCATTTGCACTGCTGATATGAGGCTTTCTTTTAAAGGCGCCAGTGCATCTCTGTC 840
DB 781 ACACCATTTGCACTGCTGATATGAGGCTTTCTTTTAAAGGCGCCAGTGCATCTCTGTC 840
QY 841 ATGATTTGAAGAACAGGAGTGGGAGGATATGTCACACCGGACCTTCAACTGGTAAAG 900
DB 841 ATGATTTGAAGAACAGGAGTGGGAGGATATGTCACACCGGACCTTCAACTGGTAAAG 900
QY 901 ACTCTCAGAGACCCAGGCACTACAGTACTATTACCTGTGTATTTCTTGGGCTTTTGC 960
DB 901 ACTCTCAGAGACCCAGGCACTACAGTACTATTACCTGTGTATTTCTTGGGCTTTTGC 960
QY 961 TGGCATCTTGGCTCTGTCTGTTTACGATGCTGCTACAGCGGTGAGAACCCAGCTCT 1020
DB 961 TGGCATCTTGGCTCTGTCTGTTTACGATGCTGCTACAGCGGTGAGAACCCAGCTCT 1020
QY 1021 ACTCCATATTGGGGGAGTGCAGCTGTGTAAGAGGGGAGGAGCAGACCTCTGTGTC 1080
DB 1021 ACTCCATATTGGGGGAGTGCAGCTGTGTAAGAGGGGAGGAGCAGACCTCTGTGTC 1080
QY 1081 GGGGCGGAGGCTTCAACCCCAACCAACCACTGTGCTTCAAGCTTCAACCCCAAGTTCA 1140
DB 1081 GGGGCGGAGGCTTCAACCCCAACCAACCACTGTGCTTCAAGCTTCAACCCCAAGTTCA 1140
QY 1141 CTGTCTCATTTCCCTTCAATCTCTGTGACCGGCTCAACTTGGAGACCTGCTGATCTC 1200
DB 1141 CTGTCTCATTTCCCTTCAATCTCTGTGACCGGCTCAACTTGGAGACCTGCTGATCTC 1200
QY 1201 CTTCCAGGAGACGGGCGGCGCCCACTTAAGAGCTGGGCGCCATCTTCCGGGGCTTCGG 1260
DB 1201 CTTCCAGGAGACGGGCGGCGCCCACTTAAGAGCTGGGCGCCATCTTCCGGGGCTTCGG 1260
QY 1261 CTTCCAGGAGACGGGCGGCGCCCACTTAAGAGCTGGGCGCCATCTTCCGGGGCTTCGG 1320
DB 1261 CTTCCAGGAGACGGGCGGCGCCCACTTAAGAGCTGGGCGCCATCTTCCGGGGCTTCGG 1320
QY 1321 CTGCGGCTTCAACCACTCTGTGACCCGAGTTTCAGAAATGAGAACCCAGCCCTCCACG 1380
DB 1321 CTGCGGCTTCAACCACTCTGTGACCCGAGTTTCAGAAATGAGAACCCAGCCCTCCACG 1380
QY 1381 CCCCCGATCAGCTGCGGAGTCCGACCCCGGAGCCCTGTACGCGGTGTGAGACGGCTGC 1440
DB 1381 CCCCCGATCAGCTGCGGAGTCCGACCCCGGAGCCCTGTACGCGGTGTGAGACGGCTGC 1440
QY 1441 CCCCCGATCAGCTGCGGAGTCCGACCCCGGAGCCCTGTACGCGGTGTGAGACGGCTGC 1500
DB 1441 CCCCCGATCAGCTGCGGAGTCCGACCCCGGAGCCCTGTACGCGGTGTGAGACGGCTGC 1500
QY 1501 GCTGTGAAGTGGAGAACCGGGGCGCACCTGCGGAGCCCAATACAGCATGTGCGGGGCT 1560
DB 1501 GCTGTGAAGTGGAGAACCGGGGCGCACCTGCGGAGCCCAATACAGCATGTGCGGGGCT 1560
QY 1561 GGGCGGCGGAGCGCGCGGCGGAGGCGAGCTGTGAGCTGTGAGGCGCGGCTCAAGG 1620
DB 1561 GGGCGGCGGAGCGCGCGGCGGAGGCGAGCTGTGAGCTGTGAGGCGCGGCTCAAGG 1620
QY 1621 ACATGAGACTGTGAGTTCCTTGAAGAAACATAGAGAGGCGCTGAGTGCAGCGCGCGCC 1680
DB 1621 ACATGAGACTGTGAGTTCCTTGAAGAAACATAGAGAGGCGCTGAGTGCAGCGCGCGCC 1680
QY 1681 TCGGCTCGGAGCCCGGCTTCTCTGTGTAGAGCCCGGCTTCCGACTGCGGGCTTCCCG 1740
DB 1681 TCGGCTCGGAGCCCGGCTTCTCTGTGTAGAGCCCGGCTTCCGACTGCGGGCTTCCCG 1740
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QY 1741 CCCTGCAAGAGGCTGCTTCTTCTGTCAGGAGCCCGGAGATCTGAGATGCC 1800
DB 1741 CCCTGCAAGAGGCTGCTTCTTCTGTCAGGAGCCCGGAGATCTGAGATGCC 1800
QY 1801 TGTGACCTCTGTTTGTGTTTCTGAGAGGAACTGTGAGAGAGAGAGAGAG 1860
DB 1801 TGTGACCTCTGTTTGTGTTTCTGAGAGGAACTGTGAGAGAGAGAGAGAG 1860
QY 1861 GATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
DB 1861 GATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 TGAAGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
DB 1921 TGAAGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
QY 1981 TGTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
DB 1981 TGTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
QY 2041 CCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
DB 2041 CCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100
QY 2101 GAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
DB 2101 GAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
QY 2161 ATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
DB 2161 ATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
QY 2221 CTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
DB 2221 CTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
QY 2281 TGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
DB 2281 TGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
QY 2341 CTTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
DB 2341 CTTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
QY 2401 CTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2440
DB 2401 CTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2440

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RESULT 2
ABQ79378
ID ABQ79378 standard; cDNA; 2440 BP.
AC ABQ79378;
DT 05-NOV-2002 (first entry)
XX
XX Bovine tumour necrosis factor receptor-1 cDNA.
XX
XX Bovine; tumour necrosis factor receptor-1; TNF-RI; antiinflammatory;
XX TNF cytotoxicity; mastitis; tumour necrosis factor-alpha; TNF-alpha;
XX monoclonal antibody B9; TNF-beta; gene; ss.
XX
XX Bos taurus.
XX
XX Key Location/Qualifiers
XX CDS 294..1709
XX FT /*tag= a
XX FT /*product= "Bovine TNF-RI"
XX FT sig_peptide 294..383
XX FT /*tag= b
XX FT /*label= signal_peptide

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FT mat_peptide 384..1706
FT /*tag= c
FT /*label= mature_bovine_TNF-RI
PN US2002076765-A1.
PD 20-JUN-2002.
XX
XX 03-OCT-2001; 2001US-0970532.
XX
XX 26-FEB-1999; 99US-122156P.
XX 25-FEB-2000; 2000US-0513007.
XX
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX Taylor MJ, Kehrli ME, Lee E, Mwangi S;
XX
XX WPI; 2002-557247/59.
XX P-PSDB; ABB98169.
XX
XX New isolated, soluble, bovine tumour necrosis factor receptor I, useful
XX for inhibiting tumour necrosis factor cytotoxicity for treating
XX mastitis, is a better inhibitor of tumour necrosis factor compared to
XX monoclonal antibody B9.
XX
XX Claim 1(a); Fig 1; 17pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding bovine tumour
XX necrosis factor receptor-1 (TNF-RI). The activity of polypeptides of
XX the invention may be described as antiinflammatory. Polypeptides of the
XX invention are useful for inhibiting TNF cytotoxicity in a bovine. This is
XX useful for treating mastitis and other inflammatory disease. Soluble
XX bovine TNF-RI is a better inhibitor of bovine TNF-alpha than monoclonal
XX antibody B9 (an antibody directed towards TNF-alpha), and can bind both
XX TNF-alpha and TNF-beta. The current sequence represents bovine tumour
XX necrosis factor receptor-1 cDNA.
XX
XX Sequence 2440 BP; 441 A; 771 C; 701 G; 527 T; 0 other;
XX
XX Query Match 100.0%; Score 2440; DB 24; Length 2440;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTTTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 60
DB 1 TTTTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 60
QY 61 TCTCTCAGCTCAAGTTTCTGAGAGCTTCTGAGAGCTTCTGAGAGCTTCTGAGAG 120
DB 61 TCTCTCAGCTCAAGTTTCTGAGAGCTTCTGAGAGCTTCTGAGAGCTTCTGAGAG 120
QY 121 GGGTTGAGAGTCTTCCGAGATGAGGCTGTGTCCTCCGAGCTTCAACCTTCACTCCC 180
DB 121 GGGTTGAGAGTCTTCCGAGATGAGGCTGTGTCCTCCGAGCTTCAACCTTCACTCCC 180
QY 181 GACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 GACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 GCGGCACTGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 GCGGCACTGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 TCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 TCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 ACCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 ACCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 CCGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

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D	b	421	CCTGTC	CCCCAAG	GA	AAAAAT	AT	TA	AA	CC	CCG	CA	AA	AT	AG	CA	CA	AT	TG	CT	GC	CA	CA	AG	TG	CC	480		
O	y	481	AC	AA	AG	T	A	C	T	A	T	G	T	A	C	A	A	T	G	A	C	T	G	A	C	T	G	540	
D	b	481	AC	AA	AG	T	A	C	T	A	T	G	T	A	C	A	A	T	G	A	C	T	G	A	C	T	G	540	
O	y	541	TG	TG	GG	CC	CT	GG	CA	CT	TA	CA	TG	CT	TG	GA	AA	CA	CT	CA	GA	CA	AG	TG	CT	G	600		
D	b	541	TG	TG	GG	CC	CT	GG	CA	CT	TA	CA	TG	CT	TG	GA	AA	CA	CT	CA	GA	CA	AG	TG	CT	G	600		
O	y	601	CC	AG	TG	CC	GG	GA	CA	AA	TG	TT	CC	AG	TG	GA	AT	TG	CG	CT	TG	TG	A	TG	GA	CC	660		
D	b	601	CC	AG	TG	CC	GG	GA	CA	AA	TG	TT	CC	AG	TG	GA	AT	TG	CG	CT	TG	TG	A	TG	GA	CC	660		
O	y	661	CT	GT	TG	CG	CT	GC	AG	AA	GA	CC	AG	T	A	CG	GA	TA	CT	GG	GT	GA	AA	CT	GG	T	720		
D	b	661	CT	GT	TG	CG	CT	GC	AG	AA	GA	CC	AG	T	A	CG	GA	TA	CT	GG	GT	GA	AA	CT	GG	T	720		
O	y	721	GT	CT	GA	CT	GC	AG	CT	CT	TG	CC	CA	TG	GC	CA	AG	T	A	T	A	T	CC	CT	TG	CC	780		
D	b	721	GT	CT	GA	CT	GC	AG	CT	CT	TG	CC	CA	TG	GC	CA	AG	T	A	T	A	T	CC	CT	TG	CC	780		
O	y	781	AC	AC	CA	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	840	
D	b	781	AC	AC	CA	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	840	
O	y	841	AT	GA	T	T	G	T	A	GA	AA	CA	AG	A	T	G	C	A	T	G	C	A	T	G	C	A	T	900	
D	b	841	AT	GA	T	T	G	T	A	GA	AA	CA	AG	A	T	G	C	A	T	G	C	A	T	G	C	A	T	900	
O	y	901	AC	T	C	T	CA	AG	A	CC	CA	AG	CA	CT	A	C	A	AG	T	A	T	A	T	CC	CT	G	T	960	
D	b	901	AC	T	C	T	CA	AG	A	CC	CA	AG	CA	CT	A	C	A	AG	T	A	T	A	T	CC	CT	G	T	960	
O	y	961	TG	GC	A	C	T	T	G	CC	CT	CT	GT	CG	CT	T	A	AG	A	T	G	C	T	A	G	C	T	1020	
D	b	961	TG	GC	A	C	T	T	G	CC	CT	CT	GT	CG	CT	T	A	AG	A	T	G	C	T	A	G	C	T	1020	
O	y	1021	AC	T	C	CA	T	A	T	T	G	CG	GA	AG	T	GA	CT	GT	GA	AA	GA	AG	GG	GA	AG	CA	MA	CT	1080
D	b	1021	AC	T	C	CA	T	A	T	T	G	CG	GA	AG	T	GA	CT	GT	GA	AA	GA	AG	GG	GA	AG	CA	MA	CT	1080
O	y	1081	CG	GC	CC	CA	GG	CT	T	CA	CC	CA	CC	CA	CA	CA	CA	CA	CA	CT	CG	CT	CA	CC	CA	AG	T	1140	
D	b	1081	CG	GC	CC	CA	GG	CT	T	CA	CC	CA	CC	CA	CA	CA	CA	CA	CA	CT	CG	CT	CA	CC	CA	AG	T	1140	
O	y	1141	CT	GT	T	CA	AT	T	CC	CC	CT	T	A	CA	T	C	T	C	T	G	A	C	CG	GT	CA	CA	CT	1200	
D	b	1141	CT	GT	T</																								

QY	1561	GGCGGCGCGCAGCGCCGCGCGGAGGCGACGCTGAGAGCTGCTGAGCGCGGCTGTCTACAGG	1620
Db	1561	GGCGGCGCGCAGCGCCGCGCGGAGGCGACGCTGAGAGCTGCTGAGCGCGGCTGTCTACAGG	1620
QY	1621	ACATGACCTGCTGCTGGTTGCTCTGAAAAACATAGAGAGCGCTGAGTGGCGCGCCCGCC	1680
Db	1621	ACATGACCTGCTGCTGGTTGCTCTGAAAAACATAGAGAGCGCGCTGAGTGGCGCGCCCGCC	1680
QY	1681	TCGGGTCCGAGCCCCGCTTCTCTGTGTAAGCCCGCCCTCCGACTGCGGCTCTCCCG	1740
Db	1681	TCGGGTCCGAGCCCCGCTTCTCTGTGTAAGCCCGCCCTCCGACTGCGGCTCTCCCG	1740
QY	1741	CCCTGAGACGGGCTGCTCTCTCTGTCAGGACGCGCGGAAAGGACTGCGAGATGCC	1800
Db	1741	CCCTGAGACGGGCTGCTCTCTCTGTCAGGACGCGCGGAAAGGACTGCGAGATGCC	1800
QY	1801	TGTGGACCTCCTGTTTTGTTTTGTTTTCTGAGAGGAAGTCTTGAGAGAGCAGCAC	1860
Db	1801	TGTGGACCTCCTGTTTTGTTTTGTTTTCTGAGAGGAAGTCTTGAGAGAGCAGCAC	1860
QY	1861	GATCTGGCAGCCACTGACCTGCTCTACTCACTAGTGTACATAGCTTTTCTCAGCTGCC	1920
Db	1861	GATCTGGCAGCCACTGACCTGCTCTACTCACTAGTGTACATAGCTTTTCTCAGCTGCC	1920
QY	1921	TGAGTGTGTCTGT	1980
Db	1921	TGAGTGTGTCTGT	1980
QY	1981	TGTGCGTGTGTGTATGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2040
Db	1981	TGTGCGTGTGTGTATGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2040
QY	2041	CCAAGGCAAGTGTGCCAAGATGAGGGGGCCCGCTTATGTCGTGTTTTTGGGCTTG	2100
Db	2041	CCAAGGCAAGTGTGCCAAGATGAGGGGGCCCGCTTATGTCGTGTTTTTGGGCTTG	2100
QY	2101	GAGAACTCAGCAAGGCACTTGGGGAACCTTACGTCGCTCCCTGAGCGGTTTCGACATAG	2160
Db	2101	GAGAACTCAGCAAGGCACTTGGGGAACCTTACGTCGCTCCCTGAGCGGTTTCGACATAG	2160
QY	2161	ATAAGCCATCTTTGTATCCACTCTGCAATCCACTCACTCACTCTGTATCACTAATAGAA	2220
Db	2161	ATAAGCCATCTTTGTATCCACTCTGCAATCCACTCACTCACTCTGTATCACTAATAGAA	2220
QY	2221	CTTTGTGCCCTGCTGCTGGAACGCTGAACGTGTCCCGAGGAGCGGGGAGACACAGAAAA	2280
Db	2221	CTTTGTGCCCTGCTGCTGGAACGCTGAACGTGTCCCGAGGAGCGGGGAGACACAGAAAA	2280
QY	2281	TGGGGCCCTCCCAAGGAGACTGCTGTCACTTCACTTCACTGCTGCTGCTGCTGCTGCT	2340
Db	2281	TGGGGCCCTCCCAAGGAGACTGCTGTCACTTCACTTCACTGCTGCTGCTGCTGCTGCTGCT	2340
QY	2341	CTTTGCGACCTGTGAATCGCAGGAGCTTCTGTAAATATACCTAAATCTTCAATTAAAG	2400
Db	2341	CTTTGCGACCTGTGAATCGCAGGAGCTTCTGTAAATATACCTAAATCTTCAATTAAAG	2400
QY	2401	CTTGCCCTGAGGAGACTGTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	2460
Db	2401	CTTGCCCTGAGGAGACTGTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	2460
RESULT 3			
ABO77487			
ID	ABO77487	standard; DNA; 2141 BP.	
XX	ABO77487;		
XX	14-MAY-2003	(first entry)	
XX	Human TNF-R DNA huTNF-R.		
XX	TNF; human; tumour necrosis factor; tumour necrosis factor receptor;		

RESULT 3	
ABQ77487	
ID	ABQ77487 standard; DNA; 2141 BP.
XX	
XX	
AC	ABQ77487;
XX	
DT	14-MAY-2003 (first entry)
XX	
DE	Human TNF-R DNA huTNF-R.
XX	
KW	TNF; human; tumour necrosis factor; tumour necrosis factor receptor;

KX	TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour; gene; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers 213..1580 /*tag= a /product= "huTNF-R"
XX	
PN	EPJ93438-A.
XX	
PD	24-OCT-1990.
XX	
PF	06-APR-1990; 90EP-0106624.
XX	
PR	21-APR-1989; 89DE-3913101.
PR	21-JUN-1989; 89DE-3920282.
XX	(BOEH ) BOEHRINGER INGELHEIM INT GMBH. (SYND ) SYNERGEN INC.
PA	
PA	Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C; MPI; 1990-321987/43. P-PsDB; ABG74755.
DR	
DR	
XX	DNA encoding TNF binding protein and TNF-receptor - used in tumour treatment and to understand mechanisms to TNF action
PT	
PS	Example 9; Fig 9; 51pp; German.
XX	
CC	This invention describes novel polynucleotide sequences encoding tumour necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP). The products of the invention are useful in pharmaceutical compositions for prophylaxis or treatment of human tumours and to understand the mechanisms of TNF action. This sequence encodes the human TNF-R, huTNF-R described in the disclosure of the invention.
CC	
CC	
CC	
CC	
CC	
SQ	Sequence 2141 BP; 455 A; 634 C; 592 G; 460 T; 0 other;
Query Match	30.2%; Score 735.8; DB 11; Length 2141;
Best Local Similarity	69.9%; Pred. No. 4,5e-141;
Matches 1152; Conservative	0; Mismatches 402; Indels 95; Gaps 8;
OY	101 GGCGCAGAGGGCTGACCTTCGAGGTGTGAAGTCTCCGATTGGGCTGTG--TTCCCCGCC 157
Db	17 GGCTCCAGTTCTGGCTTGAGGGGTTCAAGATCATCTGSGAACAAGCCGCTGATCTCATGCC 76
OY	158 CGAGTTCACCTTCACACTCCCACCAGCCGAGGCCCGGGCTTCACATGGGCATACGGAGA 217
Db	77 CGAGTTCACACCTTCACACTGTCACCCCAAAGGCACTTGGGAAGTCTTGACACAGACGAGTTC 136
OY	218 CCGTGTGCTGTCACTGTCCGGGGGGCGGCACATGCCCC AGCCCTGATGGGGATTGAAG 276
Db	137 CCGGAAACCCCGACAGACTGCGCTGCGCACACTGCTTAGCGCCAATGGGAGTGAAG 196
OY	277 GCCACAGCTGCGCCGACATCGGGCCCTCCCAACCGTGCCTGACCTGCTGTGCACATGATGC 336
Db	197 GCCATAGTGTCTGG-CATGGGCCCTCTCCACCGTACCTGACTGTGCTGCGACATGATGC 255
OY	337 TTCACGCTCTGTGGCAGATGTGTAACCCCGAGGGGTTCAAGGGCTGTGTCCCTCAACCCCG 396
Db	256 TCCTGGAGCTGTGGTGGGAATATATACCCCTCAGGGGTATTGAGATGTGTCCCTCACTAG 315
OY	397 GGGACCTGGAAGAAGAGAGAGTCCCTGTCCCCCAAGAAAATATTAACCAACCCGCAATA 456
Db	316 GGGACAGGGAAGAAGATAGTGTGTGTCCCAAGAAAAATATATTCACCTCAAAATA 375
OY	457 GCACCATTTGCTGCACCAAGTGCCCAAGAGTACTATCTGTACATGACTGTCCGGSTC 516
Db	376 ATTGATTTTGTCTGTACCAAGTGCCCAAGAGAACCTACTTGTACATATAGTCTCAAGCC 435
OY	517 CAGGGCCAGACCGGACTGCAAGGTTGTGTGCCCTTGGAACCTTACCTGCTTGGAGAAC 576

Db	CGGGGCAAGATACGACCTGCAAGGAGTGTAGAGCGGCGCTCTTCAACGCTTCAGAAAACC	495
Oy	ATCTCAGACGATGCTGAGCTGCTCCAGATGCGGAGACGAATGTTCCAGGTGAGATT	636
Db	ACCTCAGACACTGCTCAGCTGCTCCAAATGCCAAAGGAATGGGTCAAGTGAAGTCT	555
Oy	CGCTTGTGTATGTGACCGGAGCACTGTGTGCGGCTGCAGGAAGAACCACTACCGGAAT	696
Db	CTTCTTCAACGTGTGACCGGAGCACCGTGTGTGCTGCAGGAAGAACCACTACCGGAT	615
Oy	ACTGGGGTGAATCGGCTTCCGCTGTGTGAATCGACCTCTGTCCCAATGGCACATGA	756
Db	ATTGGAATGAAAACCTTTTCCAGCTTCAATGTGCAACCTCTGCTCAATGGACCGTGC	675
Oy	ATATCCCTCGCAGAGAGACAGAGACACCAATCTGCCACTGCCAATAGGCTTCTTTCTTA	816
Db	ACCTCTCTCGCAGAGAAACAGAAACACCGTGTGACTGTCCATGACAGTTCCTTTCTTA	735
Oy	AAGGCGCAAGTGCATCTCTGTCTATGATTTGAAGA--CAAGAGTGCAGAGATTAT	873
Db	GAGAAAACGAGTGTGTCTCTGTGTAGTAATGTAAAGAAACCTGAGTGCACGAAGTTGT	795
Oy	GTCCAAACCCGACCTTCACTGTGTAAACATCTCAGAACCCAGGACATACAGTATTAAC	933
Db	GCCTAACCCCAAGATTGAAATGTTAAGGCACTGAGGACTCAGGACCAACAGTGTGTGTC	855
Oy	CCCTGTGATTTGTTTGGGCTTTGCTGTGACATCTTCCGCTCTGTGATTTACATGTC	993
Db	CCCTGTGATTTTCTTTGGCTTTTGCTTTTATTCCTCTCTCTTATTTGTTAATGTATTC	915
Oy	GCTACCAACGCGTGAAGCCCAAGCTTACTTCAATGTTTGTGGGAATTCACCTGA	1053
Db	GCTACCAACGCGTGAAGTCCAAAGCTTACTTCAATGTTTGTGGGAATTCACCTGA	975
Oy	AAGAGGGGAGCCAGAA-----CTCCTGTGTCCGCGCCCAAGGCTTCAACCCACCA	1104
Db	AAGAGGGGAGGCTTGAAGAACTACTACTAGCCCTCGGCGCCCAACCAAGCTTCAGTC	1035
Oy	CCACCATCTGCTTCAAGCTCCAGCCCAAGTTCAGATCTGTCTGTCCATTCGCCCTTACATCT	1164
Db	CCACTTCCAGGCTTACCCCAACCTTGAGCTTCAAGTCCCGTCCCAATTTCAACCTTCACT	1095
Oy	CTGTGTGACCGGTCCAACTTGTGAG-----CCGTGTGATCTCCCTCCAGCAGACGG	1215
Db	CCAGCTCCACTAATACCCCGGTGTACTGTCCCAACTTGGCGGCTTCCCGCAGAGAGGTGG	1155
Oy	CCCGGCCCATCTAAGAGGTGTGGCCCATCTCTCCCGGGGCTTCCGGCTTCAACCACTCT	1275
Db	CACCAACCTAATCAGGGGGCTGACCCCATCT-----	1186
Oy	GTACCCCGGGGCTTCGGGCTCCACCACTGTGTACCCCGGGGCTTCGGGCTTCCACC	1335
Db	-----TGGACAGACCTCTGCTTCCACCC	1209
Oy	ACCTCTGACCCCGATTCAGAAAGTGAAGACCAAGCGGCCCGCCGATCAGCTCG	1395
Db	CCATCCCAACCCCTTCAAGAGTGGGAGGACAGCGCCACA---AACCACAGAGCTTAG	1266
Oy	CGATGTCCGACCCCGGACCTGTACGCGGTGTGTGACGCGCGTGCCTCCGTCGCGCTGA	1455
Db	ACACTGTATGACCCCGGACGCTGTACGCGGTGTGTGAGAAAGTGTCCCGTGTGCGCTGA	1326
Oy	AGGAGTGTGTGTGCGGCTGTGAGCTGAGCGACGACGAGATTCAGACGCTGTGAGAGA	1515
Db	AGGAATTCGTGTGCGCGCTTATGGGTGTGAGCAACAGAAATCGATCGGTGTGAGTTCAGA	1386
Oy	ACGGGCGCCACCTGTGCGAGAGCGACATGATGTGTGCGGCTGTGCGGCGGCGCACGC	1575
Db	ACGGGCGCTGTGCTGTGCGAGAGCGCAATACAGCATGTGTGCGAAGCTGTGAAGCGGCGCACGC	1446
Oy	CGCGCGCGAGGCAAGCTGTGAGTGTGTGCGCGCGCTGTCTCAAGGACATGACCTGTGTG	1635



Db 1447 CCGCGCGGAGCCACGCTGAGAGCTGTGGAGCGCTGCTCCGACATGAGACTGCTGG 1506  
Oy 1636 GTTGCTGGAAACATAGAGAGGCGCTGGGTGGCGCCGCCCTCGGTCGAGGCC 1695  
Db 1507 GCTGCTGAGAGACATCGAGAGGCGCTTGTGGCGCCGCCCTCCGCGCGGCCCA 1566  
Oy 1696 GCCTTCTCTGTGAGAGCCCGCCCTCCG 1724  
Db 1567 GTCTTCTCAGATGAGGCTGCGCCCTGCG 1595

RESULT 4  
AA006285  
ID AA006285 standard, DNA; 2141 BP.  
XX  
XX AA006285;  
XX AC  
XX 25-MAR-2003 (updated)  
DT 29-JAN-1991 (first entry)  
XX  
XX Human Tumour Necrosis Factor-Receptor cDNA insert.  
XX  
XX Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
KM LambdaTNF-R2; ratNF-R8; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT CDS 213..157  
FT /tag= a  
FT /label=hutNF-R

EP393438-A.  
XX  
XX 24-OCT-1990.  
XX  
XX 06-APR-1990; 90EP-0106624.  
XX  
XX 21-JUN-1989; 89DE-3920282.  
XX  
XX 21-APR-1989; 89DE-3913101.  
XX  
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
XX  
XX (SYND) SYNERGEN INC.  
XX  
XX Hauptmann R, Himmeler A, Maurelfoegly I, Stralowa C;  
XX  
XX WPI: 1990-321987/43.  
XX  
XX P-PSDB; AAR07451.  
XX  
XX DNA encoding TNF binding protein and TNF-receptor - used in  
XX  
XX tumour treatment and to understand mechanism to TNF action  
XX  
XX Disclosure: Fig 91(1-2); Sipp; German.  
XX  
XX ratNF-R8 (AA006284) was used to screen the HS913T cDNA library.  
XX  
XX LambdaTNF-R2 encodes the complete human TNF-R2 and was used to  
XX  
XX construct a plasmid (pADTNF-R) expressing the product the same way  
XX  
XX as pADTNF-BP (see AA006282).  
XX  
XX See also AA006282-006285.  
XX  
XX (Updated on 25-MAR-2003 to correct PI field.)  
XX  
XX (Updated on 25-MAR-2003 to correct PI field.)  
XX  
XX Sequence 2141 BP; 455 A; 633 C; 593 G; 460 T; 0 other;

Query Match 29.9%; Score 729.4; DB 11; Length 2141;  
Best Local Similarity 69.6%; Pred. No. 9,1e-140;  
Matches 1148; Conservative 0; Mismatches 406; Indels 95; Gaps 8;

Oy 101 GAGCGCAGGCTGCTCCGCGTTGAGGTCCTCGGATTTGGGCTGNG---TCCCGCC 157  
Db 17 GAGCTTCAGATTCTGGGCTTTGGGTTCAAGATCTAGGGACAGGCGGTGATCTTATCC 76  
Oy 158 CCACTTCACCTTCACCTCCCGACCCGAGGCCCGGCTCCACTGAGCATACGCGAGGA 217

Db 77 CGAGCTCAACCTCACTGTCAACCCCAAGGCACTTGGGACGTCTGGAACAGACGAGTTC 136  
Oy 218 CCGTGTGCTGCTACTGTGCGGGGCGCCACTGCCCC-AGCCCTGATGGGGATTTGAGAG 276  
Db 137 CCGGGAAGCCCCAGCACTGCGCGTGCACACTGCGCTCGAGGCCAAATGGGGAGTGAAG 196  
Oy 277 GCGACAGCTGAGCGGAGCATGGGCTCCCGACGTCGCTGCTGCTGCTGCTGCTGCTGCTG 336  
Db 197 GCGATAGCTGTCTGG-CATGGGCTCTCCAGAGTGTGCTGAGCTGTGCTGCTGCTGCTGCTG 255  
Oy 337 TTCAAGCTGTGTGAGAGATGTGACCCCGGAGGTTCAAGGCTGTGCTGCTGCTGCTGCTG 396  
Db 256 TCGTGAAGCTGTGTGGGAAATATACCCCTGAGCGTTATGAGACTGTGCTGCTGCTGCTG 315  
Oy 397 GGGACCTGAGAGAGAGAGAGTCCCTGTCGCCCAAGAAAAATATACACCGGAAAAATA 456  
Db 316 GGGACAGGAGAGAGAGATGT 375  
Oy 457 GCACCATTTGTGTCACCAAGTGGCCCAAAAGGTAATCTGTATGATGATGATGATGATGATG 516  
Db 376 ATTGATTTGTGCTGTACCAAGTGCACAAAGGAACTTACTTGTACAAATGATGATGATG 435  
Oy 517 CAGGCGAGACACGCACTGACGAGGTGTGTGCTCCCTGACCTTACAGCTTGTGAGAAAC 576  
Db 436 CCGGCGAGAGATACGCACTGACGAGAGTGTGAGAGCGGCTCTTACAGGCTTCAAGAAAC 495  
Oy 577 ATCTCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 636  
Db 496 ACCTCAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555  
Oy 637 CGCCTGT 696  
Db 556 CTTCTTGTGACAGT 615  
Oy 697 ACTGAGGTGAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 756  
Db 616 ATTGAGAGTAAACCTTTTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 675  
Oy 757 ATATCCCTGCTGAG 816  
Db 676 ACCTCTCTGCTGAG 735  
Oy 817 AAGCGCCAAAGTGTATCTCTGTATGTATGTATGTATGTATGTATGTATGTATGTATGTAT 873  
Db 736 GAGAAAGAGAGT 795  
Oy 874 GTCCAACTGACCTTCAAGTGTAAAGACTCTCAGAGCCGAGCACTACACTATTTAC 933  
Db 796 GCTAACCCCAATTCAGATGTAAAGGCACTGAGACTCAGGACACAGCTGCTGTGC 855  
Oy 934 CCGTGTGATGT 993  
Db 856 CCGTGTGATGT 915  
Oy 994 GCTACAGCGGTGAGAGCCCAAGCTTACTCATTTGTGGGCACTGAGTGTGTA 1053  
Db 916 GCTACCAAGGTGAGAGT 975  
Oy 1054 AAGAGGGGAGCCAGAA-----CTCTGTGTCGGGCGCCAGGCTTCAACCCACCA 1104  
Db 976 AAGAGGGGAGCTTGAAGAACTACTAGAGCCCTGAGCCCAACCAAGCTTCACTC 1035  
Oy 1105 CCACATCTGTGTGAGTCCAGCCCAAGTTCAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1164  
Db 1036 CCACTTCAGAGTTTACCCCACTGTGAGCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1095  
Oy 1165 CCGTGTGACCGGTTCACATTTGAGAG-----CCGTGACATCTCCCTCAGGAGAGAG 1215  
Db 1096 CCACTGTCACTATATCCCGGT 1155  
Oy 1216 CCGGCGCCCATCTAAAGGCTGCGCCCATCTCCCGGAGCTTCCGAGCTTCAACCACTCT 1275



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Db      862 TTAATGATCGCTACCAACGGTGAAGTCAAGCTCTACTCTGTTGTTGGGAAATCG 921
Qy      1044 ACTGTGTAAGAGGGGGAGCCAGAA-----CTCGGTGTCGGGCCCCAGGCTTC 1094
Db      922 ACACCTGAAAAAGAGGGGAGCTTGAAAGAACTACTACTAAAGCCCTGGCCCAAAACCA 981
Qy      1095 AACCCCAACACCATCTGCTTCAAGCTCCACCCCAAGTTCAGTCTCTCTCCATTCC 1154
Db      982 AGCTTCACTCCACCTCAGAGCTTCAACCCCACTGGGGCTTCAAGTCCCGTCCAGTTCC 1041
Qy      1155 CCTTACATCTCTGTCGAGCCGGTCCAACTTCGAG-----CCGTGCACTTCCTCC 1205
Db      1042 ACCTTCACTCCAGCTCACTATACCTCCGTACTCTCCCACTTTCGGCTCCCGC 1101
Qy      1206 AGCAGACGCGCCCGCCCTATTAAGGCTGAGCCCATCTCCGGGGCTTCGGGCTCC 1265
Db      1102 AGAGAGGTGGACCACTCATCAGGGGGCTGACCCCATCT----- 1142
Qy      1266 ACCACCTCTGTAACCCCGGGGCTCCGGGCTTCACCCACTCTGTACCCCGGGGCTCCG 1325
Db      1143 -----TGCAACAGCCCTC 1155
Qy      1326 GCCTTCACCACTCTGTGACCCCAATTGAAAGTGAAGCAGCGCCCAAGCGCCCC 1385
Db      1156 GCCTTCGACCCCATCTCCCAACCCCTTCAAGAGTGGAGAGAGGCCCAACA---AGCCA 1212
Qy      1386 GATCAGCTCGGGATGCCAGCCCGGCACTCTGACGGCTGTGAGACGGCGTCCCGC 1445
Db      1213 CAGAGCTTGAACATGATGACCCCGGCACTGTACGGCTGTGAGAAACGTGCCCGC 1272
Qy      1446 TCGGCTGGAAGAGTGTGTGGGGGCTGGAGCTGACGAGCAAGATGAGAGGGCTG 1505
Db      1273 TTGCGCTGAAGAAATGTGTGGGGGCTGAGGCTGACGAGCAAGATGATGAGGCTG 1332
Qy      1506 GAGCTGAGAAAGGAGCGGACCTGCGGAGGCGAGTACAGATCTGCGGCGCTGCGG 1565
Db      1333 GAGCTGAGAAAGGAGCGGCGCTGCGGAGGCGCAATACAGATCTGCGGCGCTGCGG 1392
Qy      1566 CGGCGCAGCGCGCGCGGAGGCGCAGCTGAGCTGTGGCGCGCTGCTCAAGGACATG 1625
Db      1393 CGGCGCAGCGCGCGCGGAGGCGCAGCTGAGCTGTGGCGCGCTGCTGCGGACATG 1452
Qy      1626 GACCTGTGGGTGTGCTGGAAGAAACATAGAGAGGAGGCTGGGTGGCGCGCGCGCTGCGG 1685
Db      1453 GACCTGTGGGTGTGCTGGAAGAAACATAGAGAGGAGGCTGGGTGGCGCGCGCGCTGCGG 1512
Qy      1686 TCCGAGCCCGGCTTCTGTGTGAAGCCCGCCCTCCG 1724
Db      1513 CCGCGCCCAAGTCTTCTCAGATGAGGCTGCGCCCTCGG 1551

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PR      19-JUN-1990; 90US-0555274.
PR      09-JUN-1993; 93US-0090366.
PR      18-JUL-1989; 89US-0381080.
PR      11-DEC-1989; 89US-0450329.
PR      07-FEB-1990; 90US-0479661.
PA      (AMGE-) AMGEN INC.
XX      Squires C, King MW, Hale KX, Brewer MT, Thompson RC;
PI      Vanderslice RW, Vannice J, Kohno T;
XX      MPI: 2001-006443/01.
DR      P-PSDB; AAB37677.
XX      Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT      non-native cysteine residue cross-linked with polyethylene glycol,
PT      useful for treating inflammatory and degenerative diseases mediated by
PT      TNF.
XX      Example 6; Fig 21; 82bp; English.
XX      The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC      (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC      novel TNF inhibitors of the present invention are useful as therapeutic
CC      agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC      for treating inflammatory and degenerative diseases mediated by TNF. The
CC      present sequence is the coding sequence for the precursor of 30 kDa TNF
CC      inhibitor. The 30 kDa TNF inhibitor can inhibit TNF alpha.
XX      Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;
SQ
Query Match 29.7%; Score 725.8; DB 22; Length 2088;
Best Local Similarity 70.0%; Pred. NO. 5e-139;
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;
Qy      148 TGTCCCGGCCCCAGTCTCAACCTTCACCTCCCGAGCCGAGGCCGCTCCACTGGGCA 207
Db      23 TCTCTAAGCCCGAATCTCAACCTTCACCTTCACCCCAAGGCACTTGGAGAGCTCTGGAC 82
Qy      208 TACCGAGAGACCGTGTGTCTCTCACTGTGCGGGGCGGCACTGCC-CAGCCCTGATGGG 266
Db      83 AGACCGAGTCCCGGAGAGCCCGACACTGCGCGCTGACCACTGCGCTGAGGCCCAATGGG 142
Qy      267 GGATTGAGAGGCAAGGTGGCGGAGATGAGGCTCCCAACGTCGTCGCTGCTGCTG 326
Db      143 GGAATGAGAGGCAATGATGCTGTGG-CATGGGCTTCTCCACCTGTGCTGACTGTGCTG 201
Qy      327 CCACTGTGCTTCCAGCTGTGTGGAGATGTATACCCCGAGGGGTTCAAGGGGCTGTG 386
Db      202 CCGGTGTGCTCCTGAGAGCTGTGTGGGAATATACCTCAGGGGTTATGACTGTG 261
Qy      387 CCTCACCCCGGGAGACTGAGAGAGAGAGAGTCCCTGTCCCAAGAAATATATACAC 446
Db      262 CCTCACCTAGGGGAGAGAGAGAGATGTGTGTGTCCCAAGAAATATATATACAC 321
Qy      447 CCGCAAAATATACCATTTGTGTGACCAAGTGCACAAAGGTACTATCTGTACATGAC 506
Db      322 CTTCAAAATATATGATTTGTGTGACCAAGTGCACCAAGAAATATATATATAC 381
Qy      507 TGTCCGGGTCCAGGGCGAGACAGGAGTGTGTGTGCGCTTGGCACTTACATGAC 566
Db      382 TGTCCAGGCGCGGGGAGAGATACGAGTGTGTGTGAGAGGGGCTTTCACCGCT 441
Qy      567 TTGAGAAACATCTCAAGCATGCTTCAAGCTGTCTCAAGTGTCCGGAGAGAAATGTTCCAG 626
Db      442 TCAGAAACCACTCAGCACTGCTCAGCTGTCTCAATATGCCAAGAAATATGCTAG 501
Qy      627 GTGAGATTTCGCTGTGTGTGAGACCGGAGCATGTGTGCTGCGTGCAGAGAAACAG 686
Db      502 GTGAGATCTTCTTGTGACAGTGAACCGGAGACCGTGTGTGTGCTGAGAGAAACAG 561
Qy      687 TACCGGAATACTGGGTGAATGAGCTTCCGATGTCTGAATCGACGCTGTGCTCAAT 746

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Db      562 TACCGGCAATTGAGTGAACCTTTTCAGTCTTCAATTGACGCTCTGCTCAAT 621
Qy      747 GGCACAGTAATAATCCCTGCGCAGAGAGACAGGACACCATTCGCACTGCAATATGAGC 806
Db      622 GGGACCGTGAACCTCTCTCCAGAGAAACAGAAACCGTGTGACCTGCAATGACGT 681
Qy      807 TTTCTTTTAAAGGCGCGCAAGTCATCTCTGTCATGATTGTAAAG--CAAGAGTGC 863
Db      682 TTTCTTTTAAAGAAACAGAGTGTCTCTGTTAGTAAAGAAACCTGAGATGC 741
Qy      864 GAAAGATTATGTCCAAACCGCACTTCAATGTGTAAGATCTCTGAGACCGACGACTACA 923
Db      742 ACCAGATTGTGCTTACCGAGATTGAAGATGTAAGGCACTGAGACTAGGACACACA 801
Qy      924 GTACTATTACCCCTGATGATTGTTCTGCGGCTTTCGCGCATTCCTGCTGTGCTC 983
Db      802 GTGCTGTGCGCCCTGGTCACTTTTCTTGTTGCTTTTATTCCTCTCTTCATTTGCT 861
Qy      984 TTAGCATGTGCTACACAGCGGTGAGACCCCAAGCTTACATTCATTTGCGGCGAGTCG 1043
Db      862 TTATGTATGCTACCAACGCTGAGAGTCCAAAGCTTACTCATTTGTTTGGGAAATCG 921
Qy      1044 ACTCTGTAAAGAGGAGGAGCCAGAA-----CTCGTGTCCGCGCCCGAGGCTTC 1094
Db      922 ACACCTGAAAAAGAGGAGGAGCTTGAAGAACTAATAAGCCCTGCGCCCAACCCA 981
Qy      1095 AACCCACCAACACCATCTGCTCAGCTCCACCCCAAGTTCCAGTCTCTTCATTTCCG 1154
Db      982 AGCTTCACTGCTCCATCCAGGCTTCAACCCCAACCTGAGCTTCCGCTGCGCAATTC 1041
Qy      1155 CTTTACATCTCTGTGACCGGTCCAACTTTCGAG-----CGTTCGATCTCTCTCC 1205
Db      1042 ACCTTCACTGCTCCAGCTCCAACTTATACCCCGGTGACTGTCCCACTTTGCGGCTCCGCG 1101
Qy      1206 AGGAGAGCGGCGCGCGCGCGCACTTAAAGCTGCGCCCACTCTCCGCGGCGCTCCGCGCTCC 1255
Db      1102 AGAGAGGTGAGCAACCTTATCAGGAGGAGCTGACCCCACTCT----- 1142
Qy      1256 ACCCACTGTATCCCGGCGCTCCGCGCTCCAGCACTCTGTACCCCGGCGCTCCG 1325
Db      1143 -----TGCCACAGCCCTC 1155
Qy      1326 GCCTTCACCACTCTGTCACACCCAGTTCAAGATGAGAAAGCCAGCGCGCGCGCC 1385
Db      1156 GCCTTCGACCCCACTCCCAACCCCTTCAAGATGAGGAGACAGCGCGCAACA---AGCA 1212
Qy      1386 GATAGCTCGGAGTGCAGACCCCGCAACCTGTATACCGGTGTGTGTGAGAGGCGTCCCGCG 1445
Db      1213 CAGAGCTTAAACACTGATGACCCCGCAACGCTGTACCGCGGTGTGTGAGAAAGTCCCGCG 1272
Qy      1446 TCGCGCTGAAAGAGTTGGTCCGCGGCTGAGGACGAGCGAGCAAGATGAGCGGCTG 1505
Db      1273 TTGGCTGTGAAAGATTTGTGTGCGGCTTAAAGGCTGAGCGAGCAAGATGATCGGCTG 1332
Qy      1506 GAGCTGAGAAACGCGGCGCACTTCGCGAGCGAGCAAGTACAGCATGCTGTGCGCGCTGCGCG 1565
Db      1333 GAGCTGAGAAACGCGGCGCTGCTGCGAGCGCAATACAGCATGCTGTGCGCGCACTGAGAG 1392
Qy      1566 CGGCGACGCGCGCGCGAGGCGCAAGTGTGAGCTGTGCGCGCGCTGTCTCAAGGACATG 1625
Db      1393 CGGCGACGCGCGCGCGAGGCGCAAGTGTGAGCTGTGCGCGCGCTGTCTCGGACATG 1452
Qy      1626 GACCTGTGAGTTGCTCTGAGAAACATAGAGAGGCGCTGGTGTGCGCGCGCGCTGTGCGG 1685
Db      1453 GACCTGTGAGTTGCTCTGAGAGCAATGAGAGAGGCGCTTTGCGGCGCGCGCGCTTCCG 1512
Qy      1686 TCCGAGCGCGCGCTTCTCTGTGTAAGCCCGCGCTCCG 1724
Db      1513 CCGCGCGCGCAAGTCTTCTCAAGATGAGGCTGCGCGCTCCG 1551

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RESULT 7  
AAZ09170

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ID      AAZ09170 standard; cDNA; 2111 BP.
AC      XX
XX      AAZ09170;
AC      XX
XX      20-MAR-2003 (updated)
DT      18-OCT-1999 (first entry)
DE      Human tumour necrosis factor binding protein cDNA.
XX      XX
XX      Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
XX      anti-inflammatory; antimetastatic; treatment; septic shock; inflammation;
XX      autoimmune glomerulonephritis; cerebral malaria; immune response;
XX      antagonist; diagnosis; de.
XX      XX
OS      Homo sapiens.
XX      XX
XX      Key
XX      CDS
XX      Location/Qualifiers
FT      187..1554
FT      /*tag= a
FT      /product= "TNF binding protein"
FT      sig_peptide
FT      187..273
FT      /*tag= b
FT      mat_peptide
FT      274..1551
FT      /*tag= c
XX      XX
XX      BP39121-A2.
XX      XX
XX      PD
XX      01-SEP-1999.
XX      XX
XX      31-AUG-1990; 99EP-0100703.
XX      XX
XX      PR
XX      12-SEP-1989; 89CH-0003319.
XX      PR      08-MAR-1990; 90CH-0000746.
XX      PR      20-APR-1990; 90CH-0001347.
XX      PR      31-AUG-1990; 90EP-0116707.
XX      XX
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      XX
XX      Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
XX      Schlaeger E;
XX      WPI; 1999-480840/41.
XX      DR      P-PSDB; AAY30934.
XX      XX
XX      New insoluble proteins, and fragments, that bind to tumor necrosis
XX      PT      factor, used to treat e.g. septic shock or cerebral malaria
XX      XX
XX      Claim 4; Fig 1; 25pp; German.
XX      PS
XX      XX
XX      This invention describes novel homogeneous insoluble proteins (I),
XX      CC      their (in)soluble fragments (Ia) and their salts that can bind tumour
XX      CC      necrosis factor (TNF). The products of the invention have
XX      CC      anti-inflammatory and antimetastatic activity. (I) and (Ia) are used (i)
XX      CC      to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
XX      CC      glomerulonephritis, cerebral malaria, immune responses and inflammation),
XX      CC      (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
XX      CC      diagnostic determination of TNF in body fluids. Antibodies raised against
XX      CC      (I) are used for affinity purification of (I). This sequence encodes
XX      CC      a tumour necrosis factor binding protein described in the method of
XX      CC      the invention.
XX      CC      (Updated on 20-MAR-2003 to correct PF field.)
XX      CC      (Updated on 20-MAR-2003 to correct PR field.)
XX      CC
XX      Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;
XX      SQ

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Query Match 29.7%; Score 725.8; DB 20; Length 2111;  
 Best Local Similarity 70.0%; Pred. No. 5e-139;  
 Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

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Qy      148 TGTCCCGCCCACTTCAACCCCTCCACTCCCGAGCCCGAGGCGCGGCTCCACTGAGCA 207
Db      41 TCTTATGCCGAGTCAACCTTCAACTGTACCTCCAGCCCAAGCACTTGGAGCTGCTGAC 100

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Oy 208 TAGCGAGGACCGTGTGCTGTACGTCGCGGGCGCCACTGATGGC -GAGCCCTGATGG 266
Db 101 AGACGGAGTCCCGGAGAGCCCGACACCTGCCCTGACACTGCCCCCTGAGCCCAATAGG 160
Oy 267 GGAATTGAGAGGCGACAGCTGCGCGGACATGAGGCTTCCCAACCGTGCCTGAGCTGCTG 326
Db 161 GGAGTGAAGAGGCGCATAGCTGTCTGG -CATGGGCTCTCCACCGTGCCTGAGCTGCTGCTG 219
Oy 327 CCACTGAGTCTTCCAGCTCTGTTGGACATGTGTACCCCGGAGGGGTTACGGGCTGGT 386
Db 220 CCGCTGGTGTCTCTGAGAGTGTGGTGAATATACCCCTCAGGGGTTATGGACCTGGT 279
Oy 387 CCTCACCCCGGGGACCTGAGAGAGAGAGAGTCCCTGCTCCCAAGAGAAATATATACAC 446
Db 280 CCTCACCTTAGGGGACAGGGAGAGAGAGATAGTGTGTCTCCCAAGAGAAATATATACAC 339
Oy 447 CCGGAAAATAGCACCAATTTGCTGACCAAGTGCACAAAGGTACCTATCTGTACATGAC 506
Db 340 CCTCAAAATATATTCGATTGTGTGTACCAAGTGCACAAAGGAACTTATGTATCAATGAC 399
Oy 507 TGTCCGGGTCCAGGGCGGAGACACGACTGTGCAAGGTGTGTGCCCTGGCACTTACATGCC 566
Db 400 TGTCCAGGCGCGGGGACAGATACGAGCTGCAAGGAGTGTGAGAGCGGCTCTTCCCT 459
Oy 567 TTGAGAACCACTCTGAGACGATGCTGAGCTGTCCAGGTGCGGGAGCAAAATGTTCCAG 626
Db 460 TCAGAAAACCACTCTGAGACCTGCTCAGCTGTCTCAATATGCCAAAGAAATGAGTACG 519
Oy 627 GTGAGATTTGGCTTGTGTAGTGTGACCGGAGCACTGTGTGCGGTGTGAGAGAAACAG 686
Db 520 GTGAGATCTCTTCTTGTGACAGTGTGACCGGGACACGTGTGTGTGACAGAAACAG 579
Oy 687 TACCGGGAATCTGGGGTGAACCTGGCTTCCGGTGTCTGAATCTGAGGCTCTGCCAAT 746
Db 580 TACCGGCAATTTGAGAGTGAACAACTTTTCCAGTGTCTCAATGAGCTCTGCTCAAT 639
Oy 747 GGCACAGTGAATATCCCTGCGAGAGAGACAGACACCATCTGCACTGCATATAGGC 806
Db 640 GGGACCGTGAACCTCTCTGCGAGAGAAACAGAACACGTGTGACCTGCGATAGCAAGT 699
Oy 807 TTTCTTTCTTAAAGGCGCAATGCTCTCTGTCTATGATTTGTAGAA--CAAGAGTGC 863
Db 700 TTTCTTTCTTAAAGAAAGAGAGTGTCTCTGTACTTAAGTAAAGAAAGCTGTGAGTGC 759
Oy 864 GAGAAGTATGTCCAAACCGACCTTCAACTGGTAAAGCTCTGAGGACCGGACGACATCA 923
Db 760 ACGAAGTGTGCTTACCCAGATTTAGATTTAGAGGACCTGAGGACCTGAGCACACA 819
Oy 924 GTACTATTACCCCTGGTATTTGCTTTCGGGCTTGGCTGTGACATCTTGCCTGTCTC 983
Db 820 GTGCTGTGCGCCCTGTGATTTTCTTTGTGCTTGTGCTTTATCCCTCTCTTCAATGGT 879
Oy 984 TTAGCATGTCCCTTACAGCGGTGTGAAAGCCCAAGCTTACTGTATTTGGGGCAGTGC 1043
Db 880 TTAATGTATCGCTTACCAACGCTGTGAAAGTCCAAAGCTTACTGTATTTGGGAAATCG 939
Oy 1044 ACTGTGTAAAGAGGGGAGCGAGAA-----CTCTGTGTCCGGGCCCAAGGCTTC 1094
Db 940 ACACCTGAAAAAGAGGGGAGCTTGAAGAACTACTATTAAGCCCTGTGGCCCAACCA 999
Oy 1095 AACCCCAACACCACTGTGCTTCAAGTCAACCCCAAGTTCAGTCTGTCTCAATGCC 1154
Db 1000 AGCTTCAAGTCCCACTTCAAGGCTTCAACCCCAACCTGTGGCTTCAAGTCCCAAGTCC 1059
Oy 1155 CTTTACATCTCTGTGACCGGTCCAACTTTCGAG-----CGTGTGATTTTCCCTCC 1205
Db 1060 ACCTTCACTCAAGTCAACCTTATACCCGAGTGTGATTCCTTTCGAGCTTCCCGC 1119
Oy 1206 AGCGAGACGGCGCGCCCATCTAAAGGCTGAGCCCATCTCCGGGGCTTCCGGGCTCC 1265
Db 1120 AGAGAGGTGAGCACCACTTATCAGGGGCTGACCCCACTCT-----1160
Oy 1266 ACCCACTCTGTACCCCGGGGCTTCCGGGCTTCAACCACTCTGTATCCCGGGGCTTCCG 1325

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Db 1161 -----TCCACAGCCCTTC 1173
Oy 1326 GCTTCACACCACTCTGACACCCAGTTTCAGAGTGTGAAAGCCAGCGCCCCAGGCGCCCC 1385
Db 1174 GCCTTCAGACCCCATATCCCAATCCCTCTTACAGAGTGTGAGAGACAGCGCCACACA---AGCCA 1230
Oy 1386 GATCAGCTCCGGATTCGCCAGTCCCGGACCTCTGTACCGCGTGTGTGACAGCGTCCCTCCG 1445
Db 1231 CAGAGCCTAGACACTGTATGACCCCGACACGCTGTATACCGCGTGTGTGAGAAAGTCCCTCCG 1290
Oy 1446 TCGGCTGTGAAGAGTGTGTGTCGCGGCTGTGAGCTGTAGCGAGCAAGATGTAGCGGCTG 1505
Db 1291 TTGGCTGTGAAGAAATTCGTTCGCGCGCTTACGAGCTGTAGCGACACAGATGTATGAGCTTG 1350
Oy 1506 GAGCTGTGAAGACGGGCGCGCACCTGCGAGGCGGACATGACATGCTGTGCGGCTGTGCGG 1565
Db 1351 GAGCTGTGAAGACGGGCGCGCTGTGCGAGGCGGAAATACAGCATGTGTGTGAGACCTTGGAGG 1410
Oy 1566 CCGGCGCACGCGCGCGCGGAGGCGACGCTGTGAGCTGTGTGCGCGCTGTCAAGGACATG 1625
Db 1411 CCGGCGCACGCGCGCGCGGAGGCGACGCTGTGAGCTGTGTGCGGACGCTGTCCGAGACATG 1470
Oy 1626 GACCTGTGAGGTTGCTGTGAAACATAGAGAGGCGCTGGTGTGCGCGCGCGCTGTGCGG 1685
Db 1471 GACCTGTGAGGCTGTGTGAGAGACATGAGAGGCGCTTTGTGCGGCGCGCGCTGTCCG 1530
Oy 1686 TCCGAGCCCGCGCTTCTGTGTGAAAGCCCGCCCTCCG 1724
Db 1531 CCGCGCGCGAGTCTTCTCAGATGAGGCTGTGCGCGCCCTCCG 1569

```

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RESULT 8
AAH4859
ID AAH4859 standard; DNA; 2111 BP.
XX
XX AAH4859;
XX AC
XX 12-NOV-2001 (first entry)
XX
XX
XX Human TNFBP-associated DNA #1.
DE
DE TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW antiprotocoll; treatment; meningococcal sepsis; cerebral malaria;
KW autoimmune glomerulonephritis; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 187..1554
FT /*tag= a
FT /*product= "TNFBP-associated protein"
FT /*tag= b
FT mat_peptide 271..1551
FT /*tag= c
XX
XX EP1132471-A2.
XX
XX 12-SEP-2001.
XX
XX 31-AUG-1990; 2001EP-0108117.
XX
XX 12-SEP-1989; 89CH-0003119.
XX 08-MAR-1990; 90CH-0000746.
XX 20-APR-1990; 90CH-0001347.
XX 31-AUG-1990; 90EP-0116707.
XX 31-AUG-1990; 99EP-0100703.
XX
XX (HOF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Brockhaus M, Dembic Z, Gentz R, Leibelauer W, Loetscher H;

```

PI Schlaeger E;  
 XX WPI: 2001-559312/63.  
 DR P-PSDB; AAB86817.  
 XX  
 PT New homogeneous, insoluble proteins that bind tumor necrosis factor  
 (TNF), useful for treating TNF-mediated disorders, e.g. inflammation  
 XX  
 XX Claim 4a; Fig 1; 26pp; German.  
 CC This invention describes novel insoluble proteins (I), also their  
 CC (in) soluble fragments and pharmaceutically acceptable salts, able to bind  
 CC tumor necrosis factor (TNF) and in homogeneous form. The products of the  
 CC invention have antiinflammatory, immunosuppressive, antibacterial,  
 CC antiprotocol activity. (I), and related recombinant proteins, are used  
 CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal  
 CC sepsis; development of autoimmune glomerulonephritis and cerebral  
 CC malaria. Also (I), or antibodies specific for them, are used for  
 CC diagnostic determination of TNF in body fluids, for affinity purification  
 CC of TNF and for identifying (ant)agonists of TNF. This sequence encodes a  
 CC human TNF binding protein described in the method of the invention.  
 CC  
 SQ Sequence 2111 BP; 447 A; 627 C; 587 G; 450 T; 0 other;  
 Query Match 29.7%; Score 725.8; DB 22; Length 2111;  
 Best Local Similarity 70.0%; Pred. No. 5e-139;  
 Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;  
 QY 148 TGTCCCGCCCGCAGTCTCAACCTCCCACTCCCGAGCCCGGCTCCACTGAGCA 207  
 DB 41 TCTCTATGCGCGAGTCTCAACCTCCCACTCCCGAGCCCGGCTCCACTGAGCA 100  
 QY 208 TACCGAGGACCGTGTGCTCTCACTGCGCGCGCCGCACTGCCC-CAGCCCTGATGAG 266  
 DB 101 AGACCGAGTCCCGGAGAGCCCGAGACATGCGCGCGCACTGCGCGCGCAATGAG 160  
 QY 267 GGATTGAGAGGCGCACAGTGGCCGAGCACTGGCCCTCCCACTGCGCGCGCTGCTG 326  
 DB 161 GGAATGAGAGGCGCACAGTGTCTGCG-CATGCGCGCTCCCACTGCGCGCGCTGCTG 219  
 QY 327 CCACTGCTGCTTCCAGCTCTGTGAGATGTATACCCCGAGGAGTTCAAGGAGCTGTC 386  
 DB 220 CCGCTGCTGCTTCCAGCTCTGTGAGATGTATACCCCGAGGAGTTATGAGCTGTC 279  
 QY 387 CTTCAACCCCGGAGCACTGAGAGAGAGAGTCCCTGTCCCAAGAAATATATACAC 446  
 DB 280 CCTCACTAGGAGGAGAGAGAGAGATGTGTGTGCTCCCAAGAAATATATACAC 339  
 QY 447 CCGCAAAATAGACACATTTGCTGACCAAGTCCCAAAAGTACTATCTGTACATGAC 506  
 DB 340 CTTCAAAATATATTTGATTTGTCTGTACCAAGTCCCAAAAGTACTATCTGTACATGAC 399  
 QY 507 TGTCCGGGTCCAGGCGGAGACAGGAGCTGAGGAGTGTGCTCCCTGACACTTACATGCC 566  
 DB 400 TGTCCAGGCGGAGGAGAGATGAGAGCTGAGGAGTGTGAGAGCGGCTCTTACCGCT 459  
 QY 567 TTGAGAGACCATCTCAGACGATGCTGCTGACAGTGCCTGGAGCGAATGTTCAG 626  
 DB 460 TCAGAAAACCATCTCAGACGATGCTGCTGACAGTGCCTGAAATGCGAAGAAATGGGTAC 519  
 QY 627 GTGAGATTTTGGCTTGT 686  
 DB 520 GTGAGATTTTGT 579  
 QY 687 TACCGGGAATAGTGGGTGAAATGAGCTTCCGAGTGTGAACTGACAGCTGTGCCAAT 746  
 DB 580 TACCGGGAATAGTGGGTGAAATGAGCTTCCGAGTGTGAACTGACAGCTGTGCCAAT 639  
 QY 747 GGCAAGTGAATATCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 806  
 DB 640 GGCAAGTGAATATCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 699  
 QY 807 TTCTTTCTTAAAGGCGCAAGTGCATCTCTGTGTATATTGTAAAGAA---CAAGAGTGC 863

DB 700 TTCTTTCTTAAAGAGAAACGAGTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 759  
 QY 864 GAGAGATTAATTCACACCCGACCTTCAACTGTGTAAAGCTCTGAGACCCAGGACATACA 923  
 DB 760 ACGAAGTGTGCTTACCCGACGATGAGAAATGTTAAGGCACTGAGGACACGACACA 819  
 QY 924 GTACTATTACCCCGT 983  
 DB 820 GTGCTGTGTGCGGCTGT 879  
 QY 984 TTAGCATGTGCTTACAGCGGTGAGAGCCCAAGCTTACTTCAATTTTGGGAGAGTCG 1043  
 DB 880 TTAATGTATGCTTACCAAGCGGTGAGAGTCCAAGCTTACTTCAATTTTGGGAGAAATCG 939  
 QY 1044 ACTGTGTAAAGAGGAGGAGCCAGAA-----CTCTGTGTGCGGCGCCCGAGCTTC 1094  
 DB 940 ACACCTGAAAAAGAGGAGGAGCTTGAAGAACTAATAAGCCCTGTGCGCCCAAAACCA 999  
 QY 1095 AACCCACACACACATCTGTGCTTCAAGCTCCACCCCAAGTTCAGTCTGTCTCATTTCC 1154  
 DB 1000 AGCTTCAAGTCCCACTCAGAGCTTCAACCCCAAGTTCAGTCTGTCTCATTTCC 1059  
 QY 1155 CTTTACATCTCTGT 1205  
 DB 1060 ACCTTCACTTCAAGCTTCACTTATACCCCGGTGACTGTCCCAATTTTGGGAGCTCCCGC 1119  
 QY 1206 AGGAGAGAGGCG 1265  
 DB 1120 AGAGAGGTGACACACCTTATACAGGAGGCTGACCCCACTCT----- 1160  
 QY 1266 ACCCACTCTGTATCCCGGAGGCTCCGAGCTTCAACCACTGTGTATCCCGGAGCTTCG 1325  
 DB 1161 -----TGGAGACGCTTC 1173  
 QY 1326 GCTTCAACCACTTGTGACCTTCAAGTTCAGAGTGTGAGAGCCAGCGCCCAAGCGCC 1385  
 DB 1174 GCTTCAACCACTTGTGACCTTCAAGTTCAGAGTGTGAGAGCCAGCGCCCAAGCGCC 1230  
 QY 1386 GATAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 1445  
 DB 1231 CAGAGCTTACACACTGTATGACCCCGGAGCTGTATGAGCTGTGTGTGTGTGTGTGTGT 1290  
 QY 1446 TCGGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 1505  
 DB 1291 TTGGGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 1350  
 QY 1506 GAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 1565  
 DB 1351 GAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 1410  
 QY 1566 CGGCGAGAGCG 1625  
 DB 1411 CGGCGAGAGCG 1470  
 QY 1626 GACCTGT 1685  
 DB 1471 GACCTGT 1530  
 QY 1686 TCGGAGCGCGCGCTTGT 1724  
 DB 1531 CCGCGCGCGAGTCTTGT 1569  
 RESULT 9  
 ID ABR84039 standard; cDNA; 2111 BP.  
 XX ABR84039;  
 AC  
 XX  
 AC  
 XX  
 DT 14-AUG-2002 (first entry)  
 XX  
 DE Human cDNA differentially expressed in granulocytic cells #610.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;  
 KW fungal infection; parasitic infection; protozoal infection;  
 KW viral infection; sterile inflammatory disease; psoriasis;  
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KW adult respiratory distress syndrome; inflammatory bowel disease;  
 KW Crohn's disease; ulcerative colitis; periodontal disease;  
 KW granulocyte activation; chronic inflammation; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200228999-A2.  
 XX  
 XX 11-APR-2002.  
 XX  
 XX 03-OCT-2001; 2001MO-US30821.  
 XX  
 XX 03-OCT-2000; 2000US-237189P.  
 XX  
 XX (GENE-) GENE LOGIC INC.  
 XX  
 XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
 XX  
 XX WPI; 2002-435328/46.  
 XX  
 XX Detecting granulocyte activation by detecting differential expression  
 XX of genes associated with granulocyte activation, which serves as  
 XX PT diagnostic markers that is useful for monitoring disease states and  
 XX PT drug toxicity -  
 XX  
 XX Claim 1; SEQ ID No 610; 11app; English.  
 XX  
 XX The invention relates to detecting (M1) granulocyte (GC) activation  
 XX (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
 XX DNA chip analysis as given in the specification, and comparing  
 XX the expression level to an expression level in an unactivated  
 XX GC, where differential expression of Gs is indicative of GCA.  
 XX Also included are modulating (M2) GA by contacting GC with an agent  
 XX that alters the expression of at least one gene in Gs; (2) screening (M3)  
 XX for an agent capable of modulating GCA or an inflammation (especially  
 XX chronic) in a tissue, an allergic response in a subject, exposure of a  
 XX subject to a pathogen or sterile inflammatory disease using the  
 XX gene expression profile; (3) detecting (M4) an inflammation (especially  
 XX chronic) in a tissue, an allergic response in a subject, exposure of a  
 XX subject to a pathogen or sterile inflammatory disease, by detecting the  
 XX level of expression of the gene in the tissue of gene(s) from Gs, where  
 XX (4) creating (M5) an inflammation (especially chronic) or in a tissue,  
 XX an allergic response in a subject, exposure of a subject to a pathogen  
 XX or sterile inflammatory disease, by contacting a tissue having  
 XX inflammation with an agent that modulates the expression of gene(s)  
 XX from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for  
 XX modulating GA; M3 is useful for screening an agent capable of modulating  
 XX GCA preferably in an inflammation in a tissue; M4 is useful for  
 XX detecting an inflammation (especially chronic) in a tissue, an allergic  
 XX response in a subject, exposure of a subject to a pathogen or sterile  
 XX inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
 XX glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal  
 XX reperfusion injury, ARDS, adult respiratory distress syndrome,  
 XX inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 XX periodontal disease; also bacterial infection, viral infection, and  
 XX parasitic infection, protozoal infection, fungal infection and M5 is  
 XX useful for treating one of the above conditions. The present  
 XX sequence represents a gene differentially expressed in granulocytes.  
 XX Note: The sequence data for this patent did not form part  
 XX of the printed specification, but was obtained in electronic  
 XX format directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 2111 BP, 445 A; 629 C; 587 G; 450 T; 0 other;  
 XX



Db	1060	ACCTTCACCTCCAGCTCCAGCTCATATACCCCGGATGATGTCCCAATTGTGGGCTCTCCCGC	1113
Qy	1206	AGCGAGACGCGCCCGCCCATCTTAAGAGCTGAGCCCATCTCTCCGGGGCTCCGAGCTCC	1285
Db	1120	AGAGAGGTGGACCAACCCCTATCAGGGGGCTACCCCATCTT-----	1160
Qy	1266	ACCCACCTCTGTACCCCGGGGCTCCGGGCTTCACCCGACTCTGTACCCCGGGGCTCCGG	1325
Db	1161	-----TGCACAGCCCTTC	1173
Qy	1326	GCCTTCACCCACTCTGTGACCCCACTTTCAGAAATGGGAAAGCCAGCGCCCGGAGCCGCC	1385
Db	1174	GCCTTCGAGACCCCATCTCCCAACCCCTTTCAGAAATGGGAGGACAGCGCCCACTA---AGCCA	1320
Qy	1386	GATCAGAGCTCGGGATGACCGACCCCGGACCCCTGTATACGGGTGTGTGTGAGACGGGTCTCCCG	1445
Db	1231	CAGAGCTTACGACTGATGATACCCCGGACGCTGTACCGCTGTGTGTGTGAGAAAGTGTCCCG	1290
Qy	1446	TCGGCTGTGAAGAGATTGTGTGGCGGCTGTGGACTGAGCGACAGACAGATTCAGCGGCTG	1505
Db	1291	TTGGGCTGTGAAGGAATTGTGTGGGGGCTTACGGCTGTAGCGACACAGATTCAGCGGCTG	1350
Qy	1506	GAGCTGTGAAGAACGGGCGCCCACTTGTGGGAGGCGCATACAGCATGTCTGGCGGCTTGCGG	1565
Db	1351	GAGCTGTGAAGAACGGGCGCTGTGCTTCGCGAGGCGCAATAACAGCATGTCTGGCGGCTTGAGG	1410
Qy	1566	CGGCGCAAGCGCGCGCGGAGGAGCCACGCTGTGAGCTGTGGGCGCGCGTTCAGGGGACATG	1625
Db	1411	CGGCGCAAGCGCGCGCGCGGAGGCCACGCTGTGAGCTGTGGGACGCGTGTCTCCGACATG	1470
Qy	1626	GACCTGTGGGTCTCTGTGAAAAATAGAGAGGCGCTGGGTGGCGCGCGCCCTTGCGG	1685
Db	1471	GACCTGTGGGTCTCTCTGTGAGAGCATGAGAGAGCGGCTTGTGGCGCGCGCCCTTGCGG	1530
Qy	1686	TCCGAGCGCGCGCTTCTCTGTGTGAAGCCCGCGCCCTTGCGG	1724
Db	1531	CCCGCGCCCACTTCTTCTAGATGAGGCTGGCGCCCTTGCGG	1569

RESULT 10

ABN95862

ID ABN95862 standard; DNA; 2111 BP.

AC ABN95862;

XX

DT 13-AUG-2002 (first entry)

XX

DE Gene #2360 used to diagnose liver cancer.

XX

KW Gene; liver cancer; db; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.

XX

OS Homo sapiens.

XX

PN WO200229103-A2.

XX

PD 11-APR-2002.

XX

PF 02-OCT-2001; 2001WO-US30589.

XX

PR 02-OCT-2000; 2000US-237054P.

XX

PA (GENE-) GENE LOGIC INC.

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX

DR WPI; 2002-426119/45.

XX

PT Diagnosing and detecting the progression of liver cancer,

PT hepatocellular carcinoma or metastatic liver tumor in a patient,

PT involves detecting the level of expression of two or more genes in a liver tissue sample

XX Claim 1, SEQ ID NO 2360; 298bp; English.

XX

CC The invention relates to a novel method for diagnosing and detecting the

CC progression of liver cancer, hepatocellular carcinoma or metastatic liver

CC tumour in a patient, and differentiating metastatic liver cancer from

CC hepatocellular carcinoma in a patient, involving detecting the level of

CC expression of two or more genes represented in ABN93503-ABN97455 in a

CC tissue sample. The method of the invention has hepatotropic, and

CC cytoskeletal activity. The method is useful for diagnosing and detecting

CC the progression of liver cancer, hepatocellular carcinoma and metastatic

CC liver carcinoma in a patient. The method is useful for identifying

CC expression profiles which serve as useful diagnostic markers as well as

CC markers that can be used to monitor disease states, disease progression,

CC drug toxicity, drug efficacy and drug metabolism.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at [http://www.int/patdb/published\\_pat\\_sequences](http://www.int/patdb/published_pat_sequences).

XX

Query Match	29.7%	Score 725.8	DB 24	Length 211
Best Local Similarity	70.0%	Pred. No. 5e-139		
Matches 1120	Conservative 0	Mismatches 387	Indels 92	Gaps 7

Qy	144	TTGCCCGGCGCCAGTCTCAACCTCTCACTCCCGACCCGAGGGCCGGGCTCCACTGGGCA	207
Db	41	TCTCTATGCCGAGTCTCAACCTTCACTGTCACTCCCAAGGCACTTGGAGCTGCTGGAC	100
Qy	208	TACGGCAGGACCGTGTGCTGTCACTGTCCGGGCGCCACTGCC - CACCCCTGAATGGG	266
Db	101	AGACCGAGTCCCGGGAGACCCACAGACTCGCGCTGCGACACTGCCCTCCAGGCCCAATGGG	160
Qy	267	GGATTGAGAGGCAACAGCTGGCCGGACATGGGGCTCCCAACCGTGCCTGGCTGTGG	326
Db	161	GGAGTGAAGGCCATAGCTGTGTGG - CATGGGCTCTCAACCGTGCTGACTGTGCTGTG	219
Qy	327	CGACTGTGTCCAGCTCTGTGGCAGATGTGTACCCCGCAGGGGTTCAAGGGCTGTGC	386
Db	220	CCGCTGTGTCTCTGGAGCTGTGTGGGAATATACCCCTCAAGGGGTATTTGAGACTGTGC	279
Qy	387	CCTCACCCCGGGACCTGGAGAAAGAGAGAGTCCCTGTCTCCCAAGAAATTTAACAC	446
Db	280	CCTCACCTTAGGGGACAGGGAGAAAGAGATATGTGTGTCCCAAGAAATTTATTCAC	339
Qy	447	CCGCAAAATAGACCATTTGCTGTGACCAAGTCCCAAGATCTATCTGTACATGAC	506
Db	340	CCTCAAATTAATTTGATTTGTCTGTATCCAAATGCCCAAGAAACCTATCTTTACATGAC	399
Qy	507	TGTCCGGGTCAGGGCGAGACACGGACTGACGGTGTGTGCCCTGTGCACCTACACTGCC	566
Db	400	TGTCCAGGCCCGGGGACAGGATACGGACTGACGGGAGTGTAGAGCCGCTCTTTCACCGCT	459
Qy	567	TTGGAGAACCAATCTCAGACGATGCTGAGCTGCTCCAGGGTCCGGGACGAAATGTTCCAG	626
Db	460	TGAGAAAACCACTCAGACACTGCTCAGCTGCTCCAAATGCCGAAAGGAATGGGTACG	519
Qy	627	GTGGAGATTTGCGCTTGTGTATGTGAACCGGACCACTGTGTGTGCGGCTGCAGAAAGAACG	686
Db	520	GTGGAGATCTCTTCTTGTGACAGTGTGAACCGGACACCGTGTGTGGCTGCAGAAAGAACG	579
Qy	687	TACCGAGAAATCTGGGGGTGAACCTGGCTTCCGGTGTGAACGTGCAGGCTCTGTCCCAT	746
Db	580	TACCGGCATTAATGAGATGAAGAAACCTTTCAATGCTTCAATTGCAAGCTCTGTCCCTCAT	639
Qy	747	GGCACAATGAAATATCCCTGCAGAGAGACAGGACCAACATCTGCCACTGCCATATGGCC	806
Db	640	GGGACCGTGCACTCTCCTGCAGAGAAACAAACACCGTGTGCACCTGCATCAGGAT	699
Qy	807	TTCTTTCTTAAGGCGCAGTGCATCTCTGTCAATGATTTGTAAAGAA --- CAAGAGTGC	863
Db	700	TTCTTTCTTAAGGAAACGAGTGTGTCTCTGTATGTAATGTAAAGAAAGCTGTGAGTGC	759

QY 864 GAGAGTTATGTCACACCGACCTTCACTGTGTAAGAAGCTCTCAGAGCCAGGACCTACA 923  
 DB 760 ACGAAGTGTGTGCTACCCCAAGATTAGAAATGTAAGGCGACCTGAGAGACTTCAGGACACACA 819  
 QY 924 GTACTATTACCCCTGGTATGTCCTTCGGGCTTTTGGCTGGAGACTCTTGCCTCTGTCTC 983  
 DB 820 GTGCTGTGGCCCTGGTCACTTTCTTTGGTCTTTTGGCTTTTATCCCTCCTCTTCAATTGGT 879  
 QY 984 TTAGCATGTCCTTACCAAGCGGTGGAAGCCCAAGCTTACTCTCATCTTTGGGGGCACTCG 1043  
 DB 880 TTAAATGTATCGCTACCAACGGTGAAGTCCAAAGCTTACTCTCATCTTTGGGGGCAAAATCG 939  
 QY 1044 ACTGTGTAAAGAGGGGAGGACCAAGAA-----CTCCGTGGTCCGCGCCCAAGCTTC 1094  
 DB 940 ACACCTGAAAAAGAGGGGAGCTTGAAGAACTACTACTAAAGCCCTTGGCCCAACCA 999  
 QY 1095 AACCCACACCAACCATCTGCTTCAAGCTTCAACCCCAAGTTCAGTCTCTTCAATTCC 1154  
 DB 1000 AGCTTCAGTCCCACTCAGAGGCTTCAACCCCAACCTTGGGGTTCAGTCCGTCGCCAGTTCC 1059  
 QY 1155 CTTTACATCTCTGTGACCGGTCACACTTCGGAG-----CCGTGCATCTCTCTCC 1205  
 DB 1060 ACCTTACCTTCCAGCTTCAACCTTATACCCCGGTGACTGTCCCACTTTGCGGCTCCCGC 1119  
 QY 1206 AGCGAGAGCGCCCGCCCATCTTAAAGGTGCGCCCATCTCCGCGGGGCTCCGGCTCC 1265  
 DB 1120 AAGAGGTGGACCAACCTTATAGGGGGTTCACCCCACTCT----- 1160  
 QY 1266 ACCCACTCTGTATCCCGGGGCTCCGCTCCACCACTCTGTATCCCGGGGCTCCG 1325  
 DB 1161 -----TCCGACACCCCTC 1173  
 QY 1326 GCCTTCACACCACTCTTCAACCCCAAGTTCAGAAAGTGGAGAGCCCGCCCGCCCGCC 1385  
 DB 1174 GCCTTCGAGCCCATCCCAACCCCTTCAAGATGGAGAGACAGGCGCCACCA--AGCCA 1230  
 QY 1386 GATCAGCTGCGGATGCGGACCCCGGACCTCTGTACGCGGTGTGAGACGCGCTGCCCG 1445  
 DB 1231 CAGAGCTTGAACATGATATACCCCGGACGCTGTAGCGCTGTGTGAGAACTGCTCCCG 1290  
 QY 1446 TCGCGCTGAGAGAGTGTGTGCGGCGCTGTGAGACTGAGCGAGCAGAGATCGAGCGCTG 1505  
 DB 1291 TTGCGCTGAGAGAAATTGCTGCGGCGCTTGAAGGCTGAGGACACAGAAATGATCGGCTG 1350  
 QY 1506 GAGCTGAGAGAGAGGCGGCACTTGGCGGAGCGGCACTAGACATGTGTGGCGCTGGCGG 1565  
 DB 1351 GAGCTGCAAGAACGGGCGCTGCTGCGCGGAGCGCATATCAGCATGTGTGCGCATGTGAAG 1410  
 QY 1566 CGGCGCAGCGCGGCGCGGAGGCAACGTAAGCTGTGGCGCGGCTGTGAGGACATG 1625  
 DB 1411 CGGCGCAGCGCGGCGCGGAGGCAACGTAAGCTGTGGAGCGCTGTCTCCGCAATG 1470  
 QY 1626 GACCTGCTGGTGTGCTTGTGAAAAATATGAGAGAGCGCTGGTGGCGCGCGCCCTCGCG 1685  
 DB 1471 GACCTGCTGGGCTGCTGTGAGGACATCGAGAGGCGCTTTGGGCGCGCCGCGCCCTCGCG 1530  
 QY 1686 TCGGAGCCCCGCTTCTGTGTGAGAGCGCGCCCTCTCG 1724  
 DB 1531 CCGCGCGCCAGTCTTCTCAGATGAGGCTGCGCCCTCG 1569

## RESULT 11

AAZ48475 standard; DNA; 2161 BP.

AAZ48475;

31-MAR-2000 (first entry)

Human tumour necrosis factor receptor (TNFR1) nucleotide sequence.

Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;

Inflammation; tumour formation; TNFR1; anticancer; ds.

XX OS Homo sapiens.  
 FN US6007995-A.  
 XX PD 28-DEC-1999.  
 XX PP 26-JUN-1998; 98US-0106038.  
 XX PR 26-JUN-1998; 98US-0106038.  
 PA (ISIS-) ISIS PHARM INC.  
 PI Baker BF, Cowbert LM;  
 DR WPI; 2000-105333/09.  
 PT Antisense inhibition of tumor necrosis factor type 1 expression for  
 PT diagnosis, treatment and prevention of disease, particularly tumors  
 XX Example 10; Columns 33-36; 34pp; English.  
 CC The invention provides antisense compounds targeted to human tumour  
 CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds  
 CC can be used in a method of inhibiting the expression of TNFR1 human cells  
 CC or tissues. The antisense compounds specifically hybridize with one or  
 CC more nucleic acids encoding TNFR1, ultimately modulating the function of nucleic  
 CC acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1  
 CC produced. The antisense compounds and method are useful as research  
 CC reagents and diagnostics, and in the treatment and prophylaxis of  
 CC infection, inflammation or tumour formation. The present sequence  
 CC represents the nucleotide sequence of human TNFR1 (Genbank Accn No:  
 CC X53313).  
 SQ Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;  
 Query Match 29.7%; Score 725.8; DB 21; Length 2161;  
 Best Local Similarity 70.0%; Pred. No. 5e-139;  
 Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;  
 QY 148 TGTCCCGCCCGCACTTCAACCTTCACTCCGACCCGAGCGCGGCTTCACTGGCA 207  
 DB 110 TCTCTATGCCGAGATCTCAACCTTCAACTGTCACCCCAAGCACTTGGGAGCTCTGGAC 169  
 QY 208 TACCGAGAGACCGTGTGTCTCACTGTCCGCGGCGCCCACTGCCC-CAGCCCTGATGGG 266  
 DB 170 AGACCGAGTCCCGGAGAGCGCCAGACCTGCGCTGCACACTGCGCTGAGCCCAATGGG 229  
 QY 267 GGATTGAGAGGCAACAGCTGCGCGGACATGAGGCTTCCCACTGTGCTGCTGCTG 326  
 DB 220 GGAATGAGAGGCAATAGTGTGTGG-CATGGGCTTCTGCACCGTGGCTGACTGTGCTG 288  
 QY 327 CCACTGTGCTTCAAGCTCTGTGTGGAGATGTATCCCGGAGGCTTCAAGGCTGCTC 386  
 DB 289 CCGCTGTGTCTCTGAGCTGTGTGGAGATATACCTTCAAGGAGTTATGTGACTGTCTC 348  
 QY 387 CCTACCCCGGGGCACTGAGAGAGAGAGTCCCTGTCCCAAGGAAATATTAACAC 446  
 DB 349 CCTACCTTGAAGGAGAGAGAGAGATGTGTGTCCCAAGGAAATATTAATCCAC 408  
 QY 447 CCGCAAAATAGACCATTTGTGTGACCAAGTGCACAAAGTACTATCTGTACATGAC 506  
 DB 409 CCTCAAAATATTTGATTTGTCTGTACCAAGTGCACAAAGTACTATCTGTACATGAC 468  
 QY 507 TGTCCGGGTCCAGGCGGAGACAGGACTGCAAGGTGTGTGCGCCCTGACCTTACATGCC 566  
 DB 469 TGTCCAGGCGCGGAGGACAGGATACGAGTGCAGGAGTGTGAGAGCGGCTCTTCAACCCCT 528  
 QY 567 TTGAGAACCATCTCAAGCATGTGCTGAGCTGTCCAGAGTCCCGGAGAGGAATGTTCAG 626  
 DB 529 TCAGAAAACCACTCAGCACTGTCTGCTTCCAAATGCCAAGAAATGGGTGAG 588-  
 QY 627 GTGAGATTTGGCTTGTGTAGTGAACCGGAGCACTGTGTGCGCTGAGAGAAACACG 686

Db 589 GTGAGAAATCTTCTTGTGACAGTGGACCGGGACACCGGTGTGGCTGAGGAAACACAG 648  
 Oy 687 TACCGGGAAATCTGGGGTGAACCTGGCTTCCGGTGTCTGAACTGACGCTTGTCCAAAT 746  
 Db 649 TACCGGCAATTAATGGAAGTGAACCTTTTCCAGTCTTCAATTCACAGCTCTGCTCTCAAT 708  
 Oy 747 GGCAAGTGAATATCCCTGCGCAGAGAGACAGACACATCTCCACCTGCGCATATGGGC 806  
 Db 709 GGGACCGTGACCTCTCTCTGCGAGAGAAACAGAACCTGTTGCACCTGCGCATGACAGT 768  
 Oy 807 TTCTTTCTTAAAGCGCGCAAGTGACCTCTCTGATGATGTTGAAGAA---CAAGAGTGC 863  
 Db 769 TTCTTTCTTAAAGAAAAGAGTGTGTCTCTCTGATGATCTTAAGAAAAGCTGGAGTGC 828  
 Oy 864 GAGAAATTATGTCCAAACCCGACTTCACTGTGAAGACTCTCAGAACCCAGGACATACA 923  
 Db 829 AACGAAGTTGTCTTACCCCAATGAGAAATGTAAAGGACATGAGGACTCAGGACACACA 888  
 Oy 924 GTACTATTAACCCCTGGTGTATGTCTTGGGGCTTTGGCTGGAGATCTTGGCTCTGTGTGC 983  
 Db 889 GTGTCTGTGGCCCCGTGTCAATTTTCTTGGTCTTGTGCCTTATATCCCTCTTCAATGGT 948  
 Oy 984 TTAGCATGTGCTTACAGCGGTGGAAGCCCAAGCTTACTGCATCATTTGCGGGCAGTGC 1043  
 Db 949 TTAATGTATGCTTACCAAGGTGAAGTCCAAAGCTTACTGTCATTTGTTGGGAAATGC 1008  
 Oy 1044 ACTGTGTAAAGAAGGGGAGCCAGAA-----CTTCTGTCCGGGCCCCAGGCTTC 1094  
 Db 1009 ACACCTGAAAAGAGGGGAGACTTGAAGGAATCTACTAATGAAGCCCTGGGCCCAACCA 1068  
 Oy 1095 AACCCCAACACATCATGTGCTTCAAGCTTCAACCCCAAGTTCAGTCTGTCTCAATGCC 1154  
 Db 1069 AGCTTCAGTCCCATCTCCAGGCTTCAACCCCACTTGGGCTTCAAGTCCGTGCCCAATGCC 1128  
 Oy 1155 CCTTACATATCTCTGTGACCGGTCCAACTTGGGAG-----CGGTGCATCTCCCTGC 1205  
 Db 1129 ACCTTCACTTCAAGCTTCACTTATACCCCGGTGTGCTGCCAATTTGGCGGCTCCCGC 1188  
 Oy 1206 AGCGAGACGCGCCCGCCCATCTTAAAGGCTGGCCCATCTTCCGGGGCTCCGAGCTCC 1265  
 Db 1189 AGAAGAGTGGGACCAACCTTATCAGGGGGCTAACCCCATCT----- 1229  
 Oy 1266 ACCCACTCTGTACCCCGGGGCTTCCGGGCTTCCAGCCACCTTGTATCCCGGGGCTTCCG 1325  
 Db 1230 -----TGCGACAGCCCTC 1242  
 Oy 1326 GCTTCCACCCACTCTGTGACCCCACTTGAAGTGGGAAGCAAGCGCCGCCAGCGCCCC 1385  
 Db 1243 GCTTCCGACCCCATCTCCCAACCCCTTCAAGATGGGAGGACAGCGCCACAA---AGCA 1299  
 Oy 1386 GATCAGCTCGCGGATGCGGACCCCGCGGACCTGTATACGGGATGTGGAGACGCGTCCCGG 1445  
 Db 1300 CAGAGCTTACACTGTATGACCTCCGCGACGCTGTACGCCGTGTGTGAAGAACGTGCCCGG 1359  
 Oy 1446 TCGCGCTGAAGAGATTGGTGCAGCGGCTGTGGAATGAGCGACACAGATGAGCGGCTG 1505  
 Db 1360 TTGGGCTGGAAGGAATTTGTGCGGGGCTTAAGGGCTGAGCGACACAGATGAGATCGGCTG 1419  
 Oy 1506 GAGCTGGAAGACGGGCGCCACTCTGCGCGAGCGCGCATGACGATGTCTGGCGGCTGCGG 1565  
 Db 1420 GAGCTGCGAAGACGGGCGCTGTGCTGCGCGAGCGCAATCAACATGCTGGCACTGGAAG 1479  
 Oy 1566 CGGGCGAAGCGCGCGCGGAGGCAACGTGAGAGCTGTGGGCGCGGTCTCAGGGACATG 1625  
 Db 1480 CGGGCGAAGCGCGCGCGGAGGCAACGTGAGAGCTGTGGGACGCGTGTCTCGGACATG 1539  
 Oy 1626 GACCTGTCTGGTTGCTCTGGAAGAAACATAGAGAGCGCTGTGGTGGCGCGCCGCTCGCG 1685  
 Db 1540 GACCTGTCTGGCTGTCTGGAAGACATGAGAGAGGCGCTTTGGGGCCCGCGCTCTCCG 1599  
 Oy 1686 TCCGAGCCCCCTTCTTGTGTGAAGCCCCCGCTTCCG 1724

Db	1600	CCCGGCCCAAGTCTTCACATGAGGCTGGCCCCCTGGC	1638
<b>RESULT 12</b>			
XX	ID	ABT04971	
XX	AC	ABT04971; standard; DNA; 2161 BP.	
XX	DT	11-OCT-2002 (first entry)	
XX	DE	Cyclokin tumor necrosis factor (TNF) polynucleotide SEQ ID No 1.	
XX	KW	Antisense compound; tumour necrosis factor receptor 1; liver disease;	
XX	KW	TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;	
XX	human; ds.		
XX	OS	Homo sapiens.	
XX	PM	WO200248168-A1.	
XX	PD	20-JUN-2002.	
XX	PF	22-OCT-2001; 2001WO-US51224.	
XX	PR	24-OCT-2000; 2000US-0695451.	
XX	PA	(ISIS-) ISIS PHARM INC.	
PI	Baker BF, Cowser LM, Zhang H, Dean NM;		
DR	WPI: 2002-583481/62.		
DR	P-PsDB; AAO22286.		
PT	Novel antisense compound targeted to nucleic acid molecule encoding		
PT	tumor necrosis factor receptor 1 (TNFR1), useful for treating humans		
PT	having disease associated with TNFR1 e.g. hepatitis, liver injury,		
PT	liver cancer -		
PS	Example 10; Page 69-71; 121pp; English.		
XX	The invention relates to an antisense compound 8 to 30 nucleotides in		
CC	length targeted to nucleic acid molecule encoding tumour necrosis factor		
CC	receptor 1 (TNFR1), where the antisense compound inhibits expression of		
CC	TNFR1. The antisense compound is useful for inhibiting the expression of		
CC	TNFR1 in cells or tissues. The antisense compound is also useful for		
CC	treating an animal (preferably human) having a disease or condition		
CC	associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver		
CC	injury) or a hyperproliferative disorder such as cancer, by inhibiting		
CC	the expression of TNFR1. The antisense compound is useful for		
CC	diagnostics, therapeutics, prophylaxis and as research reagents and kits.		
CC	This polynucleotide sequence represents a human nucleic acid sequence		
CC	relating to the TNFR1 of the invention.		
SQ	Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other:		
Query Match	29.7%; Score 725.8; DB 24; Length 2161;		
Best Local Similarity	70.0%; Pred. No. 5e-139;		
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 77;			
QY	148 TGTCGCCGCCCAAGTCTTCACCTTCACCTCCGACCCGAGGCCCGGCTCCACTGGACA	207	
Db	110 TCTGTATGCCGAGTGCTCACCCCTCACTGCACCCCAAGCACTTGGAGTGCTCTGAC	169	
QY	208 TAGCGAGAGACCGTGTTCTGTCTACTGTCTCGGGGCGGCACTTGCCC-CAGCCCTGATGGG	266	
Db	170 AGACCGAATCCCGGGAACCCCAAGACCTGCGGCCCACTGCGCCGAAATGGG	229	
QY	267 GGATTGAGAGGCCACAGCTGGCCGGAACATGGAGCCCTCCCAACGTAAGCTGAGCTGCTGCTG	326	
Db	220 GAGTAGAGAGCCATAAGCTGTCTGG-CATGGAGCTCTTCACCTGAGTCTGATCTGTCTG	288	
QY	327 CCACGTGTCCTTCAGACTCTTGTGGCAATGTATACCAGGAGGATTCAAGGGCTGTGCT	386	



CC combination of a death domain receptor ligand and a diterpenoid  
 CC triepoxide. This method has cytostatic activity and works by blocking  
 CC TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the  
 CC invention may be used for treating tumours, particularly solid tumours,  
 CC e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma  
 CC also neurological malignancies, haematocytic malignancies, e.g.  
 CC non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant  
 CC cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma,  
 CC lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia,  
 CC bullous pemphigoid, discoid lupus erythematosus, lichen planus. The  
 CC combination may be administered with other active agents, e.g. anti-  
 CC metastatic, anti-tumour or anti-angiogenic agents. The potent synergy  
 CC between the diterpenoids and the death domain ligands allows increased  
 CC killing at equivalent or lower doses, and can sensitize otherwise  
 CC resistant cells. This sequence represents the human tumour necrosis  
 CC factor alpha receptor (TNF-R1) DNA. TNF-R1 is a death domain receptor  
 CC used in the used method of the invention in combination with diterpenoid  
 CC triepoxides to kill tumours by inducing apoptosis.

XX Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;

Query Match 29.7%; Score 725.8; DB 24; Length 2161;

Best Local Similarity 70.0%; Pred. No. 5e-139; Mismatches 387; Indels 92; Gaps 7;

Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

QY 148 TGTCCCGCCCGCACTTCAACCTTCACTCCCGACCCGAGGCCCGGCTTCCACTGGGCA 207  
 DB 110 TCTCTATGCGCCGAGTCTCAACCTTCACTGTCACCCCAAGGCACTTGGAGAGCTCTGAC 169  
 QY 208 TACGCGAGGACCGCTGTGTCTCTCACTGTGCGGGCCCGCACTGCC-CAGGCTGATGGG 266  
 DB 170 AGACCGAGTCCCGGAGAGCCCGACACTGCGCTGCCACACTGCTGAGGCCCAATGGG 229  
 QY 267 GATTTGAGAGGCGCAGACTGGGCGGACATGAGGCTCCCGACCTGTGCTGCTGCTG 326  
 DB 230 GGAATGAGAGGCGCAGACTGGGCGGACATGAGGCTCCCGACCTGTGCTGCTGCTG 288  
 QY 327 CCACTGTGTCTTCCAGCTCTGTGAGAGATGTATACCCCGAGGGGTTTCAAGGGCTGCT 386  
 DB 289 CCGCTGTGTCTTCCAGCTCTGTGAGAGATGTATACCCCGAGGGGTTTATGAGCTGCTC 348  
 QY 387 CTTCAACCCCGGAGCCTGAGAGAGAGAGAGTCCCTGTCCCAAGAGAAATATATACAC 446  
 DB 349 CTTCAACCTTAGGGGAGAGAGAGAGATGTGTGTGTCCCAAGAGAAATATATATACAC 408  
 QY 447 CCGGAAATATGACATTTGTGTGACCAAGTGCACAAAGGTACTTATGTATATATGAC 506  
 DB 409 CTTCAAAATATTTGATTTGTGTGACCAAGTGCACAAAGGTACTTATGTATATATGAC 468  
 QY 507 TGTCCGGGTCCAGGGCGAGACCGGACTGAGGGTGTGTGCTCCCTGGCACTTACATGCC 566  
 DB 469 TGTCCAGGGTCCAGGGCGAGAGTGTGAGAGAGTGTGAGAGGGCTCTTACCGCT 528  
 QY 567 TTGAGAAACATCTCAACGATGCTGAGTGTCTCAAGTGTCCGGGAGCAAAATTTCCAG 626  
 DB 529 TCGAAAAACCACTCAAGCACTGTCTCAAGTGTCTCAAAATGCCAAAGAAATGGTCTAG 588  
 QY 627 GTGAGATTTTGTGCTGT 686  
 DB 589 GTGAGATTTTGTGCTGT 648  
 QY 687 TACCGGAAATATGCTGGGTGAAACTGTGCTTCCGAGTGTGTGAACTGACCTGTGCCAAT 746  
 DB 649 TACCGGCAATATGAGATGAGAAACCTTTTCCAGTGTGTGCAATTTGACGCTGTGCTCAT 708  
 QY 747 GGCAGATGAATATCTCCCTGCGAGAGAGAGAGACATCTGCCATCTGCATATATGGGC 806  
 DB 709 GGGACCTGTGACCTCTCTGCGAGAGAAACAGAAACCTGCTCACTGCGCATGACAGGT 768  
 QY 807 TTTCTTTCTTAAAGGCGCAAGTGCATCTCTGTGATGATGTATAGAA---CAAGAGATGC 863  
 DB 769 TTTCTTTCTTAAAGAAACGAGTGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828

QY 864 GAGAAATTATGTCCAAACCCGACCTTCACTGTGTAAAGACTCTCAAGACCCAGGACCTTCA 923  
 DB 829 ACCAAATGTGTGCTTACCCCGAGTGTGAGAAATGTAAAGGCACTAGAGACTCAGGACACCA 888  
 QY 924 GTACTATTACCCCGGAGATTTGCTTCCGGCTTTGCTGAGCAATCTTCCCTGCTGTGCTG 983  
 DB 889 GTGCTGTGCTTCCCGGAGTGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 948  
 QY 984 TTAGCATGTGCTTACAGCCGCTGAGAGCCCAAGCTTACTTCAATCTTGTGCGGCACTGC 1043  
 DB 949 TTATGTATGTGCTTACAGAGCGTGTGAGAGTGTCAAGCTTACTTCAATTTGTGTGAAATCG 1008  
 QY 1044 ACTCTGTAAAGAGGGGGAGCCAGAA-----CTCTGTGCTCCGCGCCCAAGGCTTC 1094  
 DB 1009 ACACTGTAAAAAAGAGGGGGAGTGTAAAGAACTACTTAAAGCCCTGCGCCCAAAACCA 1068  
 QY 1095 AACCCCAACCAACATCTGCTTCAAGTGTCAAGCCCAAGTGTCAAGTGTCTGTCAATGCC 1154  
 DB 1069 AGCTTCACTCCCACTCAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCC 1128  
 QY 1155 CTTTACATCTCTGTGTGACCGGTCCAACTTGTGAG-----CCGTGATCTCTCTCC 1205  
 DB 1129 ACCTTCACTCTCAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCC 1188  
 QY 1206 AGCAGAGCGCCCGGCGCCCACTTAAAGGCTGTGCGCCCAATCTCTCCGCGGCTCTCC 1265  
 DB 1189 AGAGAGGTGTGACCACTTCAAGGGGGGTGAGCCCACTCT----- 1229  
 QY 1266 ACCCACTCTGTATCCCGGGGCTCTCGGCTCTCAAGCACTCTGTATCCCGGGGCTCTCG 1325  
 DB 1230 -----TGTGACAGCTCTC 1242  
 QY 1326 GCTTCAACCCACTCTGTGACCCCGAGTTTCAAGATGTGGAAGCCAGCGCCCGAGCGCCCG 1385  
 DB 1243 GCTTCAACCCACTCTGTGACCCCGAGTTTCAAGATGTGGAAGCCAGCGCCCGAGCGCCCG 1289  
 QY 1386 GATCACTGTGCGAGATGTGCGAGCCCGGCACTTGTATCGGGTGTGAGCGGCTGTGCCCG 1445  
 DB 1300 CAGAGCTGTAGACATGTATGACCCCGGCACTGTATCGGGTGTGAGCGGCTGTGCCCG 1359  
 QY 1446 TCGGCTGTGAAAGATGTGTGCGGCGCTGTGAGCTGAGGAGAGAGATGTGAGCGGCTGT 1505  
 DB 1360 TTGCGCTGTGAAAGATGTGTGCGGCGCTGTGAGCTGAGGAGAGAGATGTGAGCGGCTGT 1419  
 QY 1506 GAGGTGAGAAACCGGGGCGCACTGTGCGAGGCGGAGTGTGAGAGATGTGAGCGGCTGT 1565  
 DB 1420 GAGGTGAGAAACCGGGGCGCTGTGCGAGGCGGAGTGTGAGAGATGTGAGCGGCTGT 1479  
 QY 1566 CCGGCGCAACCGGCGCGCGGAGGCGCACTGTGAGCTGTGAGGCGGCTGTGAGGAGCATG 1625  
 DB 1480 CCGGCGCAACCGGCGCGCGGAGGCGCACTGTGAGCTGTGAGGCGGCTGTGAGGAGCATG 1539  
 QY 1626 GACTGTGTGAGTGTGCTGTGAGAAACATGAGAGAGCGCTGTGAGGCGGCTGTGAGGCG 1685  
 DB 1540 GACTGTGTGAGTGTGCTGTGAGAGAGATGTGAGAGAGCGCTGTGAGGCGGCTGTGAGGCG 1599  
 QY 1686 TCGGAGCCCGGCTTCTGTGAGAGCGGCGGCTGTGAGGCGGCTGTGAGGCGGCTGTGAG 1724  
 DB 1600 CCGGCGCAACCGGCTTCTGTGAGAGCGGCGGCTGTGAGGCGGCTGTGAGGCGGCTGTGAG 1638

RESULT 14  
 ID AA090513 standard; DNA; 2175 BP.  
 XX AA090513;  
 AC 19-JAN-1996 (first entry)  
 DT 19-JAN-1996 (first entry)  
 XX p55 TNF-R gene.  
 DE p55 TNF-R gene.  
 XX p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;  
 KW epidermal growth factor receptor; EGF-R; protease; inhibitor;

KW phorbol myristate acetate; PMA; 88.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 256..1623 /tag= a  
 FT CDS /product= p55 TNF-R  
 FT 2143..2149 /tag= b  
 FT mlec\_signal /note= "possible poly-A signal"  
 FT  
 FT  
 PN AU9475742-A.  
 PD 04-MAY-1995.  
 XX  
 XX 11-OCT-1994; 94AU-0075742.  
 XX  
 XX 12-OCT-1993; 93IL-0107268.  
 XX  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 PA  
 PI Backin M, Brakebusch C, Varfolomeev E, Wallach D;  
 DR WP1; 1995-194342/26.  
 DR P-PSDB; AAR75084.  
 XX  
 XX  
 PT New protease capable of cleaving soluble tumour necrosis factor  
 PT (TNF) receptor - from cell-bound TNF- receptor, useful for  
 PT antagonising deleterious effects of TNF.  
 PT  
 PS  
 PS Disclosure: Fig 1; 40pp; English.  
 XX  
 XX This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.  
 CC Expression of this receptor is regulated by shedding of the  
 CC extracellular receptor fragment. The p55 TNF-R can be shed in response  
 CC to different inducing agents, e.g. phorbol myristate acetate (PMA),  
 CC depending on cell type. The only region of the receptor whose structure  
 CC affects the shedding response is the spacer region (see AAR75012) in the  
 CC extracellular domain. This region is located close to a site of cleavage  
 CC of the molecule, and links the Cys rich module to the transmembrane  
 CC domain. The spacer region of the encoded protein was used to create the  
 CC chimeras between human p55 TNF-R and murine epidermal growth factor  
 CC receptor (EGF-R) that are represented by AAR75007-11. This spacer region  
 CC was subjected to deletion mutations (AAR75013-25) and substitutions  
 CC (AAR75026-47). Of the spacer region, the most important residues are  
 CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most  
 CC important of these. The shedding of the receptor is independent of the  
 CC side chain identity of these residues, with the exception of a limited  
 CC dependence on the identity of Val 173. Mutations which alter the  
 CC conformation of the protein adversely effect the shedding process. The  
 CC mutations shown in AAR75013-47 were introduced in order to create an  
 CC inhibitor of a protease that is capable of cleaving the soluble TNF-R  
 CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in  
 CC AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease  
 CC inhibitors can be used for enhancing TNF function.  
 CC  
 XX Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T; 0 other;  
 SO  
 Query Match 29.7%; Score 725.4; DB 16; Length 2175;  
 Best Local Similarity 69.6%; Pred. No. 66-139;  
 Matches 1128; Conservative 0; Mismatches 401; Indels 92; Gaps 7;

Db 230 GAAGTAGAGGCCAADAAGCTGTCTGG -CATGGGCGCTTCCACGTCGCTGACCTGCTGCTG 288  
 Qy 327 CCACGTGGTCTTCCAGCTCTGTGGCAGATGTGTATCCCGGAGGGGTTCAAGGGCTGTGTC 386  
 Db 289 CCGCTGGTGTCTCCGAGCTGTGTGGGAAATATACCCCTGAGGGGTTATGTGACTGTCTC 348  
 Qy 387 CCTCACCCCGGGGACCTGAGAGAGAGAGAGTCCCTGTCCCAAGGAAATATTAACAC 446  
 Db 349 CCTCACCTTAGGGGACAGAGAGAGAGAGATGTGTGTGTCTCCCAAGGAAATATATCCAC 408  
 Qy 447 CCGCAAAATAGCACATTTGTGTGACCAAGTGCCCAAAAGGTACTTATCTGTACAAATGAC 506  
 Db 409 CCTCAAAATATATTTGATTTGTGTATACCAAGTGCCCAAAAGGAACTACTTGTACAAATGAC 468  
 Qy 507 TGTCCGGGTCCAGGGCCAGAGACAGGACTGTGAGGGTGTGTGCTCCCTGTGACCTTACCTGCC 566  
 Db 469 TGTCCAGGCGCGGGGACAGATACGACTGTGAGGGAGTGTGAGCGGTCTCTTACCGCT 528  
 Qy 567 TTGGAGAACATCTCAGACGATGCTGAGCTGTCCAGTGTCCGGGACGAATGTTCAG 626  
 Db 529 TCAGAAAACACCTCAGACACTGTCTCAGCTGTCTCAAAATGCCAAGGAAATGGTCTAG 588  
 Qy 627 GTGAGATTTGCGCTTGTGTAGTGTGACCGGACACTGTGTGCGGCTGAGGAAGAACAG 686  
 Db 589 GTGAGATCTTCTTGTGACAGTGAGACCGGGACACCGGTGTGTGCTGAGGAAGAACAG 648  
 Qy 687 TACCGGAAATCTGGGGTGAATCTGGCTCCGGTGTCTGAATCTGACCTGTCTCCAT 746  
 Db 649 TACCGGCAATTAATGAGAGAAACCTTTTCCAGTCTTCAATTCAGCTGTGCTCAAT 708  
 Qy 747 GGCAAGAGTAATATCCCTGCGAGAGAGACAGACACATCTGCACTGACATATGAGGC 806  
 Db 709 GGACACGTGACACTCTCTGCGAGAGAAACAGAACACCGTGTGACACTGTGCAATGACGT 768  
 Qy 807 TTTCTTTTAAAGGCGCCCAAGTGCATCTCTGTGATATGTAAAGAA---CAAGAGTGC 863  
 Db 769 TTTCTTTTAAAGAGAAACGAGTGTGTCTCTGTGTATCTTAAGAAAGCTGTGAGTGC 828  
 Qy 864 GAGAAATTAATGCAACCCGACTTCAACTGTAAAGCTCTGAGGACCGGAGCACTACA 923  
 Db 829 ACGAAGTGTGCTTACCCAGATTTAGAGATTTAAGGCACTGAGACTCGGACCAACA 888  
 Qy 924 GTACTATTACCCCTGTGATTTGTCTTGGGCTTTGCTGCGATCTTGCCTGTGCTGTC 983  
 Db 889 GTGCTGTTGCCCTGTGATTTTCTTTGGTGTGCTTTATCCCTCTTCAATGGT 948  
 Qy 984 TTACATGTGTCTTACCAAGGCTGGAAGCCCAAGCTTACTCATCTATTTGCGGAGTGC 1043  
 Db 949 TTAATGTATGCTTACCAACGCTGGAAGTCCAAAGCTTACTCATTTGTTGGGAAATGC 1008  
 Qy 1044 ACTGTGGTAAAGAGGGGAGCCAGAA-----CTCCTGTGTCGGGCGCCAGGCTTC 1094  
 Db 1009 ACACCTGAAAAGAGGGGAGCTTGAAGAACTACTTAAGCCCTTGAGCCCAAAACCA 1068  
 Qy 1095 AACCCACCAACACATCTGCTTCAAGCTTCAACCCCAAGTTTCAAGTCTGTCTTCCATCC 1154  
 Db 1069 AGCTTCAGTCCCATCCAGGCTTCAACCCCAAGCTTCAAGTCTGTCTTCCATCC 1128  
 Qy 1155 CCTTACATCTCTGTGACCGGTCAACTTGGAG-----CGGTGCAATCTCTCC 1205  
 Db 1129 ACCTTCACTCTCACTCACTCACTTAAACCCCGGTACTGTCCAACTTGTGCGGCTCCGC 1188  
 Qy 1206 AGCAGAGCGGCGCGCCCATCTAAAGCTGTGGCCCATCTCCGCGGGGCTCCGCGCTCC 1265  
 Db 1189 AGAAGGTGGACCACTTATCAGGGGCTGTAACCCCATCT----- 1229  
 Qy 1266 ACCCACTCTGTACCCCGGAGCTTCCGAGCTTCAACCAACTTGTACCCCGGAGCTTCCG 1325  
 Db 1230 -----TGGACAGCCCTTC 1242  
 Qy 1326 GCTTCAACCACTCTGTGACCCCACTTCAAGATGGGAGACCAAGCGCCCAAGCGCCCTCC 1385  
 Db 1243 GCTTCCGACCCCAATCCCAACCCCTTTCAGAAATGGGAGGACAGCGCCCAACA---AGCCA 1299

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QY 1386 GATCAGCTCGCGAATCCGACCCCGGACCTCTACGCGGTGTGAGACGCGTCCCGG 1445
DB 1300 CAGAGCCCTAGACACTGATGATACCCCGGACGCTGTACGCGGTGTGAGAACGTGCCCCC 1359
QY 1446 TCGGCTGTGAGAGAGTTGTGCGGCGGCTGTGAGACGACGACGAGATGAGAGGCTG 1505
DB 1360 TTGGGCTGTGAGAGAGTTGTGCGGCGGCTGTGAGACGACGACGAGATGAGAGGCTG 1419
QY 1506 GAGCTGTGAGAACGCGGCGGCTGTGCGGCGGCTGTGAGACGACGAGATGAGAGGCTG 1565
DB 1420 GAGCTGTGAGAACGCGGCGGCTGTGCGGCGGCTGTGAGACGACGAGATGAGAGGCTG 1479
QY 1566 CCGGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1625
DB 1480 CCGGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1539
QY 1626 GACCTGTGAGAGAGTTGTGCGGCGGCTGTGAGACGACGAGATGAGAGGCTG 1685
DB 1540 GACCTGTGAGAGAGTTGTGCGGCGGCTGTGAGACGACGAGATGAGAGGCTG 1599
QY 1686 TCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1745
DB 1600 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1659
QY 1746 C 1746
DB 1660 C 1660

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## RESULT 15

AAQ10955 standard; cDNA; 2111 BP.

AAQ10955;

09-JAN-2003 (updated)

24-MAY-1991 (first entry)

Encodes human 55kD TNF-binding protein.

Tumour Necrosis Factor; binding proteins; septic shock;

autoimmune glomerulonephritis; lymphokine; cytokine.

Homo sapiens.

Key

sig\_peptide

mat\_peptide

EP417563-A.

20-MAR-1991.

31-AUG-1990;

20-APR-1990;

12-SEP-1989;

08-MAR-1990;

(HOFF) HOFFMANN-LA ROCHE AG.

Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;

Schlaeger EU;

WP1; 1991-081851/12.

P-PSDB; AAR11082.

Insoluble tumour necrosis factor binding proteins - and DNA

encoding them, useful in pharmaceutical prods. and for antibody

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PT prodn.
PS Claim 4; Fig 1; 26pp; German.
XX Partial amino acid sequences were determined for the 55 and 75kD
CC TNF-BPs (see AAR1072-R11081) and oligonucleotide primers were
CC synthesised based on these partial sequences. The primers were used
CC to produce a cDNA fragment for use as a probe to screen a human
CC placental cDNA bank constructed in lambda g11. Positive clones were
CC identified and sequenced. DNA constructs comprising the TNF-BP coding
CC sequence may also contain a fragment encoding a human Ig domain.
CC Recombinant constructs are used to transform cells to confer
CC improved TNF-binding properties.
CC See also AAQ10956.
CC (Updated on 09-JAN-2003 to add missing OS field.)
SQ Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T; 0 other;

Query Match 29.74; Score 724.2; DB 12; Length 2111;
Best Local Similarity 70.04; Pred. No. 1,1e-138;
Matches 1119; Conservative 0; Mismatches 388; Indels 92; Gaps 7;

QY 148 TGTCCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 207
DB 41 TCTATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 100
QY 208 TACGCGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 266
DB 101 AGACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 160
QY 267 GAGTTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 326
DB 161 GAGTTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 219
QY 327 CCACTGTGCTTCCAGCTCTGTGAGATGTGTATACCCCGGAGGCTTCAAGGCGTCTG 386
DB 220 CCGCTGTGCTTCCAGCTCTGTGAGATGTGTATACCCCGGAGGCTTCAAGGCGTCTG 279
QY 387 CCTCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 446
DB 280 CCTCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 339
QY 447 CCGGAAATATGACCACTTTGCTGTGACCAAGTGTGCAAAAGTATCTGTATCAATGAC 506
DB 340 CCTCAAAATATGACCACTTTGCTGTGACCAAGTGTGCAAAAGTATCTGTATCAATGAC 399
QY 507 TGTCCGCTTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 566
DB 400 TGTCCGCTTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 459
QY 567 TTGGAGAACCATCTCAGACGATGCTGAGCTGCTCCAGGCGGCGGCGGCGGCGGCGGCGG 626
DB 460 TCAGAAACCATCTCAGACGATGCTGAGCTGCTCCAGGCGGCGGCGGCGGCGGCGGCGG 519
QY 627 GTGAGATTTGCGCTTGTGTAGTGAACCGGAGACCTGTGTGCGGCTGTGAGAGAACG 686
DB 520 GTGAGATTTGCGCTTGTGTAGTGAACCGGAGACCTGTGTGCGGCTGTGAGAGAACG 579
QY 687 TACCGGAAATATGAGGCTGAACTGCTTCCGCTGTGAACTGACGCTGTGCTCAAT 746
DB 580 TACCGGAAATATGAGGCTGAACTGCTTCCGCTGTGAACTGACGCTGTGCTCAAT 639
QY 747 GGCACAGTGAATATCCCTGCGCAGGAGACGAGACCACTGCGCACTGCGCAATATGGGC 806
DB 640 GGCACAGTGAATATCCCTGCGCAGGAGACGAGACCACTGCGCACTGCGCAATATGGGC 699
QY 807 TTTCTTTTAAAGCGCGCAAGTATCTCTGTATGATTTGAAGAA---CAAGAGTGC 863
DB 700 TTTCTTTTAAAGCGCGCAAGTATCTCTGTATGATTTGAAGAA---CAAGAGTGC 759
QY 864 GAGAAATTATGTCCAAACCGCACTTCACTGTGTAAGACTCTCAGACCGCACTTACA 923
DB 760 ACAGAAATTATGTCCAAACCGCACTTCACTGTGTAAGACTCTCAGACCGCACTTACA 819

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OY 924 GTACATTAACCCCTGGTGAATTTGCTTCGGGCTTGGCTGGCATCCTTGCCCTGTGCTC 983
DB 820 GTGCTGTGCCCCCTGGTCAATTTCTTTGGTGTGGCTTTTATCCCTCTTCAATGAT 879
OY 984 TTACGATGTGCTTACACGCGGTGAGGCCAAGCTCTACTCCATCATTTTGGCGAGTCG 1043
DB 880 TTAATGATCGGTACCAAGGTGGAAGTCCAAAGCTCTACTCATTTGTTGGGAAATCG 939
OY 1044 ACTGTGTAAAGAGGGGAGCCAGAA-----CTCCTGTGTCGGGCCCCAGGCTTC 1094
DB 940 ACACCTGAAAAAGAGGGGAGCTTGAGAGAACTACTAAGCCCCCTGCCCCAAACCCA 999
OY 1095 AACCCACACACACCATCTGCTTGCAGTCCACCCCAAGTTCAGTCTGTCTCCATGCC 1154
DB 1000 AGCTTCAGTCCCATCTCCAGGCTTCACCCCCACCCCTGGGCTTCAGTCCGATGCCAGTTC 1059
OY 1155 CTTTACATCTCCTGTGACCGGTCCAACTTTCGAG-----CCGTGCAATCTCCCTCC 1205
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OY 1206 AGCGAGACGGCCCCCCCCATTTAAAGCTGAGCCCCATCTCCGGGGCTTCGGGCTTC 1265
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OY 1266 ACCCACCCTGTGACCCGGGGGCTCGGGCTCCACCCACCTGTGACCCCGGGGCTCCG 1325
DB 1180 GACC----- 1183
OY 1326 GCCTTCACCCACCTCTGACCCCACTTGAGAAAGTGGAAAGCCAGCCGCCAGCCGCC 1385
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OY 1386 GATCAGCTCGGGAATGCCGACCCCGGACCTGTACGCGGTGTGGACGGCGTGCCTCCG 1445
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Search completed: September 15, 2003, 05:11:31  
Job time : 483 secs





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DB 421 CCTGTCCCAAGAAAATATACACCCGAAAATGCAACATTGCTGACCAAGTGTCC 480
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DB 901 ACTCTCAGAGACCCAGGCACTACAGTACTAATTAACCCCTGAGTATGTCTTGGGCTTTGCC 960
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DB 1621 ACATGAGACTGCTGGGTTGCTCTGAGAAAACATAGAGAGAGCCCTGAGTGTGAGCGCGCC 1680
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DB 1861 GATCTGCGAGCACTGACCTGTGTCTACTCACTCAGTGTACATAGCTTTTCTCAGTGTCC 1920
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DB 1921 TGAAGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
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DB 1981 TGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
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DB 2041 CCAAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100
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DB 2101 GAGAACTCAGCAAGGCGACTTGGGGAACTTACGTCGCTGAGCGGCTTGTGCGAGTAG 2160
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DB 2281 TGGGGCTCTCCCAAGGAGTAGCTGTTCAGTTCACTGCTGCTGCTGCTGCTGCTGCT 2340
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DB 2401 CTCTGCTCTGAGAGGAGCTGTGTAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2440
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RESULT 2  
US-08-321-668-1  
Sequence 1, Application US/08321668  
Patent No. 565859  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSH, Cord  
APPLICANT: VARPOLOMEY, Eugene  
APPLICANT: BARKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
NUMBER OF SEQUENCES: 42  
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/321,668  
FILING DATE: 12-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH-13  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2175 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 256..1620  
US-08-321-668-1  
Query Match 29.8%; Score 727; DB 1; Length 2175;  
Best Local Similarity 69.6%; Pred. No. 5,4e-150;  
Matches 1129; Conservative 0; Mismatches 400; Indels 92; Gaps 7;  
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DB 1300 CAG 1359  
QY 1446 TCGGCTGT 1505  
DB 1360 TTGGCTGT 1419



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QY 1155 CCTTACACTCTCTCTGTGACCGGTCCAACTTGCAGAG-----CCGTGCAATCTTCCCTCC 1205
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QY 1746 C 1746
Db 1660 C 1660

RESULT 4
US-08-126-016-1
: Sequence 1, Application US/08126016
: Patent No. 5811261
: GENERAL INFORMATION:
: APPLICANT: WALLACH, DAVID
: APPLICANT: NOPHAR, YARON
: APPLICANT: KEMPER, OLIVER
: APPLICANT: ENGELMANN, HARTMUT
: APPLICANT: BRAKEBUSCH, CORD
: APPLICANT: ADERKA, DAN
: TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
: TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-1)
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Broadway and Neimark
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:

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1      APPLICATION NUMBER:  US/08/126,016
2      FILING DATE:  24-SEP-1993
3      CLASSIFICATION:  435
4      PRIOR APPLICATION DATA:
5      APPLICATION NUMBER:  US 07/625668
6      FILING DATE:  13-DEC-1990
7      ATTORNEY/AGENT INFORMATION:
8      NAME:  BROWDY, ROGER L
9      REGISTRATION NUMBER:  25,618
10     REFERENCE/DOCKET NUMBER:  WALLACH4
11     TELECOMMUNICATION INFORMATION:
12     TELEPHONE:  202-628-5197
13     TELEFAX:  202-737-3528
14     TELEX:  248633
15     INFORMATION FOR SEQ ID NO:  1:
16     SEQUENCE CHARACTERISTICS:
17     LENGTH:  2175 base pairs
18     TYPE:  nucleic acid
19     STRANDEDNESS:  single
20     TOPOLOGY:  linear
21     MOLECULAR TYPE:  CDNA
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23     NAME/KEY:  CDS
24     LOCATION:  256..1620
25     FEATURE:
26     NAME/KEY:  mat_peptide
27     LOCATION:  319..1620
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29     US-08-126-016-1

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	Best Local Similarity	69.6%;	Pred. No. 5,4e-150;			
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Qy	208	TACCCGAGGACCGGTGTGCTGTCACTGTCGCGGGCCGCGCACTGGCC-C-CAGCCCTGATGGG	266			
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Qy	267	GGATTGAGAGGCCACAGCTGGCCGAGACATGGGGCTTCCCACTGTCCTGGCTCTGCTG	326			
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Qy	327	CCACTGGAGTCTCCAGCTCTGTTGGCAGATGTGTACCCCGAGGGGCTTCAAGGGCTGTGTC	386			
Db	289	CCGCTGTGCTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTC	348			
Qy	387	CCTCAACCCCGGGGACCTGGAGAGAAGAGAGTCCCTGTGCCCAAGAAAAATATACAC	446			
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Qy	447	CCGAAAAATGACCACTTTGTGTGACCAAGGACCAAAAGGTAACTATCTGTACAAATAC	506			
Db	409	CCTCAAAATATTTGATTTGCTGTACCAAGTCCCAAAAGAACCTTCTGTACATGAC	468			
Qy	507	TGTCCTGGTCCAGGGCGAGACACGGACTGCAGGGTGTGTGCCCTTCGACCTACCTGCC	566			
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Db	529	TCAGAAAAACACTTAGACACTGTGCTTCAGCTGTCTCCAAATGCCAGAAAGGAAATGGGTGAC	588			
Qy	627	GTGAGATTTTGCTTGTGTGTGTGAGACCGGGACACTGTGTGCGGCTGCGAGAAAGAACAG	686			
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1300 CAGAGCTTACAGACATGATGACCCCGGACGCTGTACGCGGTGTGGAAGAGTGCCTCG 1359
1446 TCGGCTGGAAGAGTGTGTGCGGCGCTGGAAGTGAAGCAGACGAGATCGAGCGCTG 1505
1360 TTGCGCTGGAAGAAATGTGTGCGGCGCTGAGGCTGAGCGACACAGATCGATCGGCTG 1419
1506 GAGCTGGAAGAGCGGCGGACCTGTGCGGAGGCGAGTACAGATGCTGTGCGGCTGTGCG 1565
1420 GAGCTGGAAGAGCGGCGGCTGTGCGGAGGCGCAATACAGATGCTGTGCGGCTGTGCG 1479
1566 CGGCGCAGCGCGCGCGGAGGCGACGCTGTGAGGCTGTGCGGCGGCTGTGAGGAGCATG 1625
1480 CGGCGCAGCGCGCGGAGGCGACGCTGTGAGGCTGTGCGGCGGCTGTGAGGAGCATG 1539
1626 GACCTGTGAGTGTGTGGAAGAAATAGAGAGGCGCTGTGAGGCGCGCGCTGTGCG 1685
1540 GACCTGTGAGTGTGTGGAAGAAATAGAGAGGCGCTGTGAGGCGCGCGCTGTGCG 1599
1686 TCGGAGCGCGCGCTGTGTGTGGAAGCGCGCTGTGAGTGTGAGGCGCTGTGCGCGCTGTG 1745
1600 CCGCGCGCGCGCTGTGTGTGGAAGCGCGCTGTGAGTGTGAGGCGCTGTGCGCGCTGTG 1659
1746 C 1746
1660 C 1660

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RESULT 5
US-08-054-970-1
; Sequence 1, Application US/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054,970
; FILING DATE: 03-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1620
; US-08-054-970-1

Query Match 29.8%; Score 727; DB 4; Length 2175;
Best Local Similarity 69.6%; Pred. No. 5,4e-150;
Matches 1129; Conservative 0; Mismatches 400; Indels 92; Gaps 7;

148 TGTCCCGCCCGAGTCTCAACCTCCCACTCCCGACCCGAGGCGCGGCTGCACTGAGCA 207
110 TCTCTATGCGCCGAGTCTCAACCTCTCAACTGTACACCCCAAGCACTTGGAGCTGTGAC 165
208 TACGCGAGAACCGTGTGTGTGCTGCTGTCGCGGCGCGCACTGCCC-CAGCCCTGATGG 266
170 AGACCGAGTCCCGGGAAGCCCAAGCACTGCGCGCTGCGACACTGCTGAGCCCAATGGG 229
267 GATTTAGAGAGCCACAGTGTGCGGAGATGGGCTTCCCAACCGTGTGCTGTGCTGTG 326
230 GAGGTGAGAGCCATACACTGTGTG-CATGGGCTTCTTCAACCGTGTGACTGTGCTGTG 288
327 CCACTGTGCTTCCAGTGTGTGTGCGAGATGTGTACCCCGAGAGGTTTCAAGGGGCTGTG 386
289 CCGGTGTGCTTCTGAGAGCTGTGTGTGTGGAATATACCCCTCAGAGGTTATTTGACTGTG 348
387 CTTCAACCCCGGAGACTGTGAGAGAGAGAGAGTCCCTGTGCCCAAGGAAATATTAACAC 446
349 CTTCACTTAAAGGAGCAGAGGAGAGAGATGATGTGTGTGCTCCCAAGGAAATATATCAC 408
447 CCGGAAATATAGACATTTTGTGTGACCAAGTGTGCAAAAGTACTATCTGTACATGAC 506
409 CTTCAAAATATTTGATTTGTGTGTACCAAGTGTGCAAAAGGAACTTACTGTACATGAC 468

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Oy	507	GTGTCGGGTCACGAGGCGAGACACGCACTGACAGGGGTGTGGCCCTGGACCTTACACTGACC	566
Db	469	TGTCAGGAGCCCGGAGCAGGATACCGACTGACAGGAGTGTGAGACGGCTCTTCAACGGCT	528
Oy	567	TTGGAGAACCACTTCAGACGATGCGCTGAGCTTCAGGTGCGGAGCGAATGTTCCAG	626
Db	529	TCAGAAAACCACTTCAGACACTGCTCAGCTGCTCCAAATGCGGAAGAAATGGGTCAAG	588
Oy	627	GTGAGATTTGGCCTTGTGTGATGTGACCCGGGACACTGTGTGCGGTGTGAGAGAAAGAACAG	686
Db	589	GTGAGATCTTCTTCTTGACAGTGGACCGGAGACCGGTGTGCTGTGACGAGAAACACAG	648
Oy	687	TACGGGGAATACCTGGGAGTGAATCGGCTTCGGGTGTGAACCTGACGCTGTGCCAAT	746
Db	649	TACGGCAATTATTGAGATGAATACTTTTCCAGTGTCTTCAATTGACCTTGTGCTCAAT	708
Oy	747	GGCACAGTGAATATCCCTGCGCAGAGAGACAGGACACCAATCTGCACATGCACTATATGAGC	806
Db	709	GGGACCGTGACCTCTCCTGCGCAGGAGAAACAGAACCGTGTGACCTGCGCATGACAGGT	768
Oy	807	TTCTTTCTTAAAGCGCGCAAGTGCACTCTCTGTCAATGATTGTAGAA--CAAGAGTGC	863
Db	769	TTCTTTCTTAAAGAGAAACGAGTGTCTCTGTAGTAATGTAAAGAAAGCTGTGAGTGC	828
Oy	864	GAGAAGTATATGCCAACCGGACCTTCCACTGTGTAAAGCTCTCAGGACCCAGGCACTTCA	923
Db	829	ACGAAGTGTGTCTTACCCCAATGAGATGTAAAGGCACTGAGGACTTCAGGCACACCA	888
Oy	924	GTACTATTACCCCTGGTATGTTCTTCCGGGCTTTGGCTGTGAGCACTTCCTGCTGTGCTC	983
Db	889	GTGCTGTGCCCTGTGTCTATTTCTTGGTCTTTTGTGCTTTTATCCCTCTCTTCAATGGT	948
Oy	984	TTAGCATGTGCTATCCAGCGGTGGAAGCCCAAGCTTACTTCATCTTTCGGGCAAGTGG	1043
Db	949	TTAATGTATGCTATCCAAACGGTGAAGTCCAAAGCTCTACTCATGTTGTGGGAAATCG	1008
Oy	1044	ACTGTGTAAAGAGGGGAGGCAAAA-----CTCCGTGTCCGGGCCCCAGGCTTC	1094
Db	1009	ACACTGTAAAGAGGGGAGGCTTAAAGAACTACTTAAGCCCTTGAGCCCAACCA	1068
Oy	1095	AACCCACACACCAATCTGCTTTCAGTTCACCCCAAGTCCAGTCTGTCTCCATTGCC	1154
Db	1069	AGCTTCAATGCCCACTTCAGAGCTTCAACCCCACTCGGGCTTCAGTCCGTGCCAGTTC	1128
Oy	1155	CTTTCATCTCTGTGACCGGTCCAATTCGGAG-----CCGTGCATCTTCCCTCC	1205
Db	1129	ACCTTCACTCGACGTCCACCTATACCCCGGTGACTGTCCCAATTTTGCGGCTCCCGC	1188
Oy	1206	AGCGAGACGGCCCGCCCATTTAAAGGTGCGCCCATCTTCGCCGGGCTTCGGGCTTC	1265
Db	1189	AGAGAGGTGGCACCACTTATACGGGGGTGACCCCATCT-----	1229
Oy	1266	ACCACTCTGTGATCCCGGGGCTTCGGGCTCAACCACTCTGTATCCCGGGGCTTCGG	1323
Db	1230	-----TGCACAGCCTTC	1242
Oy	1326	GGCTTCAACCACTCTGTGACCCCAAGTTCAAGTGGGAAGCCAGCGCCCAAGCGCCCTC	1385
Db	1243	GGCTTCGAGCCCATTCGCCAACCCCTTCAAGATGGGAGAACAGGCCCAACA--AGCA	1299
Oy	1386	GATCAAGCTGCGGAGATGCCGACCCCGGACCTGTATACGGGTGTGTGAACGGGTGCCCTCG	1445
Db	1300	CAGAGCTTACACATGATGACCCCGGACGCTGTACCGCTGTGTGAGAAACCTGCCCCG	1355
Oy	1446	TGCGGCTGGAAGAGTGGTGTGGGGGCTGGGACTGAGGAGACAGATGTGAGGCGCTG	1509
Db	1360	TTGCGCTGGAAGAAATTCGTGCGGGGCTTAGGGCTGAGGCAACACAGATGTGATGCGCTG	1419
Oy	1506	GAGCTTGAAGAACGGGCGCAGCTTGTGCGAGGCGCAATACAGCATCTGACGCGCTTGGCGG	1565
Db	1420	GAGCTTGAAGAACGGGCGCTGCTGTGGCGGAGGCAATACAGCATCTGCGCGACTTGGAGG	1479
Oy	1566	CGGCGCACGCGCGCGCGAGGCGACAGCTGTGAGCTGTGTGGCGCGGCTGTCAAGGACATG	1622

Db	1480	CGGGGCAAGCGCGCGCGCGAGAGCCACGCTGGAGTGTCTGGGAGCGCGTGTCTCGGACATG	1539
Qy	1626	GACCTGCTGGGATTGCTCTGGAAAAACATAGAGAGCGCTGGGTGGCCGCCGCCCTCGCG	1685
Db	1540	GACCTGCTGGGCTGTCCCTGGAGAGCATGAGAGGCGCTTTGGCGGCCGCCCTCTCCG	1599
Qy	1686	TCCGAGCCCCGCCCTTCTCTGTGTGAAGCCCGCCCTCGCACTGGCGGAGCTCCCGCCTG	1745
Db	1600	CCCGCGCCCAAGTCTTCTCAGATGAGGCTGGCGCCCTCGCGGAGCTCTTAGAACCGTCTTG	1659
Qy	1746	C 1746	
Db	1660	C 1660	

  

Qy	327	CCACTGGTCTCCACGCTCTGTTGGCAGATGTATACCCCGAGGGGTTCAAGGAGCTGGCT	386
Db	230	GGAAGAGAGGCAATAGCTGTCTGG-CATGGGCTCTCTCAACCGTGTCTGACCTGTGCTG	288
Qy	267	GGATTGAGAGGCCACAGCTGGCCGGGACATYGGGCTTCCCACTGGTCTGGCTGTGCTG	326
Db	170	AGACCGAATCCCGGGAAGCCCGACAGCATGTGCGCTGCACACTTGCCTTAGGCCAAATGG	229
Qy	208	TACGGAGAGACCGATGTTGTCTGTCATCTGTGCGGGCGGCACTGGCC-CAGCCCTGATGG	266
Db	110	TCTCTATGCCCCGAAGTCTTCAACCTTCAACTGTGCACCCCAAGGACACTTGGGAGTCTTGAC	169
Qy	148	TGTCCCCCGCCCACTGTCTAACCCTTGCACATCTCCCGACCCGAGAGCCCGGAGCTCACTGGGA	207
Db	110	TCTCTATGCCCCGAAGTCTTCAACCTTCAACTGTGCACCCCAAGGACACTTGGGAGTCTTGAC	169
Qy	29.7%	Score 725.8; DB 3; Length 2161;	
Best Local Similarity	70.0%;	Pred. No. 9.9e-150;	
Matches 1120;	Conservative	0; Mismatches 387; Indels 92; Gaps 7;	

  

US-09-106-038A-1	
US-09-106-038A-1	
Sequence 1, Application US/09106038A	
Patent No. 6007995	
GENERAL INFORMATION:	
APPLICANT: Brenda F. Baker and Lex M. Cowsett	
TITLE OF INVENTION: ANTISENSE MODULATION OF TNFRI	
TITLE OF INVENTION: EXPRESSION	
NUMBER OF SEQUENCES: 91	
CORRESPONDENCE ADDRESSES:	
ADDRESSEE: 1615 Pharmaceuticals, Inc.	
STREET: 2292 Faraday Avenue	
CITY: Carlsbad	
STATE: CA	
COUNTRY: U.S.A.	
ZIP: 92008	
COMPUTER READABLE FORM:	
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: Windows NT	
SOFTWARE: Microsoft Word 97	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/09/106.038A	
FILING DATE: June 26, 1998	
CLASSIFICATION: 514	
ATTORNEY/AGENT INFORMATION:	
NAME: Laurel Spear Bernstein	
REGISTRATION NUMBER: 37,280	
REFERENCE/DOCKET NUMBER: RTS-0004	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: (760) 931-9200	
TELEFAX: (760) 603-3820	
INFORMATION FOR SEQ ID NO: 1:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 2161	
TYPE: nucleic acid	
STRANDEDNESS: single	
TOPOLOGY: linear	





[illegible]

Qy	1566	GGGGGACACGGCGCGCCGAGAGCCACGCTGAGGTGCTGGAGCCGCGTGCACAGGACATG	1625
Db	1480	CGGGGACACGGCGCGCCGAGAGCCACCGCTGAGGTGCTGGAGACCGGTGCTCCGGAATG	1539
Qy	1626	GACCTGCTGGGTTGCTGTGAAAAATAGAGAGGCGCTGGGTGCGCGCCGCCCTCGCG	1685
Db	1540	GACCTGCTGGGCTGCTGTGAGAGACATGAGAGAGGCGCTTTTGCGGGCCCCCGCCCTCCG	1599
Qy	1686	TCCGAGCCCGCCCTTCTCTGTGAGGCGCGCCCTTCG	1724
Db	1600	CCCGGCCCACTTCTTCATATAGAGCGCGCCCTTCG	1638

RESULT 8  
US-08-050-319B-24  
; Sequence 24, Application US/08050319B

GENERAL INFORMATION:  
APPLICANT: M.Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: PatentIn Release #1.0, version #1.25

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INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:

LENGTH: 2062 base pairs

STRANDEDNESS: double

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;      TOPOLOGY: linear
;
;      MOLECULE TYPE: cDNA to mRNA

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FEATURE:

LOCATION: 155..1519

42-9676-000-80-80

Query Match	29.5%
Best local similarity	69.4%

Matches 1123; Conservative

148 TGTCCCGGCCAGTCTCA

Db 9 TCTCTATGCCGAGTCTCAACCTCAACTGTCACCCCAAGGCACTTGGGACGTCCTGGAC 68

Qy	208	TACGCGAGGACCGCTGTTGGTGTCACTGTCGCGGGCGGCACATGCC - CAGCCCTTAATGGG	266
Db	69	AATCCGATGCTCCGGGAAAGCCGACACTGCGGTGCACATCTGCCCTTAGGCCCAATGGG	128
Qy	267	GGATTGACAGGCGCACAGCTGGCGCGACATGGGCTCCCAACCTGCTGGCTGGCTGGCTGG	326
Db	129	GAGGTGAGGGCGCATAGCTGTCTGG - CAATGGCTCTTCCACCGTGTATACCTGCTGCTG	187

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QY 327 CCACGTGCTTCCAGCTCTGTTGGCAGATGTGTACCCCGCAGGGGTTCAGGGGCTGTGTC 386
DB 188 CCGCTGATGCTCTGGAGCTGTGGGAAATATACCCCTCAGGGGTTCATGAGCTGTGTC 247
QY 387 CCTCACCCCGGGGACCTGGAGAGAGAGAGAGTCCCTGTCCCAAGAAATATACAC 446
DB 248 CCTCACCTAGGGGAGAGAGAGAGAGATAGTGTGTCTCCAGAGAAATATATCCAC 307
QY 447 CCGCAAAATATGACCACTTGTCTGACCAAGTGCACAAAGTACCTATCTGTACATGAC 506
DB 308 CCGCAAAATATGCTGATTTGTCTGTACCAAGTGCACAAAGAACTACTGTATGACATGAC 367
QY 507 TGTCCGGGTTCAGAGGGGAGAGACAGGACTGAGGGGTGTGGCCCTGGGACCTACATGACC 566
DB 368 TGTCCAGGCCCCGGGGAGAGATAGAGACTCAGAGAGATGTAGAGAGGCTCTTCAACGGT 427
QY 567 TTGGAGAACCATCTCAGACGATGCTGAGCTGTCCAGGTGCGGGAGCGAAATGTTCCAG 626
DB 428 TCAGAAACCACTCAGACATGCTCAGCTGTCCAAATGCGAAAGAAATGGGTGAG 487
QY 627 GTGGAGATTTGGCTTGTGTAGTGAACCGGAGCACTGTGTGCGGTGCGAGAAAGACAG 686
DB 488 GTGGAGATCTCTTCTTGTGACAGGTGACGCGGACACCGTGTGTGCTGCGAGAAAGACAG 547
QY 687 TACCGGGAATACTGGGGGTGAAACTGGCTTCCGGTGTCTGAACTGAGGCTCTGTCCCAT 746
DB 548 TACCGGCAATATTGGAGTGAACCACTTTCCAGTGTCTTCAATGGAGCTCTGTCTCAT 607
QY 747 GGCACAGTGAATATATCCCTCTGCGAGAGAGACAGACCATCTGCTACCTATATGGGC 806
DB 608 GGGACCGTGCACCTCTCTGCGAGAGAGAAACAGAACCGTGTGTGACCTGCGCATCAGGT 667
QY 807 TTTCTTTTAAAGGGGCGCAAGTGCATCTCCGTGTATGATGTGAAGAA---CAAGAGTGC 863
DB 668 TTTCTTTTAAAGAGAAAGAGTGTGTCTCTGTAGTATGTAAAGAAAGCCTGAGTGC 727
QY 864 GAGAGATTATGTCAACCCGACCTTCAACTGTGAAGACTCTCAGAGACCCAGGCACTACA 923
DB 728 ACGAAGTTGTGCTACCCCAATGAGATGTAAAGGACCTGAGGACTCAGGACACCA 787
QY 924 GTACTATTAACCCCTGTGTATGTCTTGGGGCTTTGCTGGCATCTTGGCTCTGTGCTC 983
DB 788 GTGCTGTGGCCCTGTGTATTTCTTGTGTCTTGTCTTAACTCTCTCTCTTCAATGAT 847
QY 984 TTAGCATGTGCTATCAGCGGTGAGAGCCAGCTCTACTCATCATTTGGGGGAGTGC 1043
DB 848 TTAATGTATCGTACCAACGTTGGAAGTCAAGCTCTCATTTGTTGGGAAATGC 907
QY 1044 ACTCTGTAAAGAGGGGAGCCAGAA-----CTCTGTGTCCCGGCCCAAGCTTC 1094
DB 908 ACACCTGAAAAAGGGGGAGCTTGAAGAACTACTAATAAGCCCTGTGCCAAACCA 967
QY 1095 AACCCCAACACCATCTGCTTCAAGCTCCACCCCAAGTTCATCTCTGTCTTCAATCCC 1154
DB 968 AGCTTCAATCTCCATCCAGGCTTCAACCCCAACCTGTGGCTTCAATCTCTGTCCAGTCC 1027
QY 1155 CTTTACATCTCTGTGACCGGTTCACAACTTCCGAG-----CCGTGCAATCTCCCTCC 1205
DB 1028 ACCTTCACTCTCAGCTCAGCTAATACCCCGGTATACCTGTCCCAACTTTGGCGCTCCCGC 1087
QY 1206 AGCAGAGAGGCGCGCCCATCTTAAAGGCTGGCCCATCTCTCCGGGGCTCTCCGCTCC 1265
DB 1088 AGAAGAGGGGAGCAACCTTATCAGGGGGCTGACCCCATCT----- 1128
QY 1266 ACCCACTCTGTACCCCGGGGCTCCGCGCTCCACCACTCTGTACCCCGGGGCTCTCC 1325
DB 1129 -----TGGACAGCCCTC 1141
QY 1326 GCTCTCAACCACTCTGTGACCCCAAGTTTCAAGATGGAGAGCAGCGCCCAAGCGCCCC 1385
DB 1142 GCTCTCAACCCCACTCTGTGACCCCAAGTTTCAAGATGGAGAGCAGTGTCCAC---AGCCA 1198

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QY 1386 GATCACTCTCGGATGCCGACCCCGGACCTGTATACCGGATGTGAGCAGCGTGCCTCCG 1445
DB 1199 CAGAGCTTAGACACTGATGACCCCGGACGCTGTACCGCCGTGTGTGAGAAAGTGCCTCCG 1258
QY 1446 TCGGCTGGAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1505
DB 1259 TTGCGCTGAAAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1318
QY 1506 GAGCTGAGAAAGGAGCGGCTACCTGCGAGAGCGGAGTACAGCATGTGTGTGTGTGTGTGT 1565
DB 1319 GAGCTGAGAAAGGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1378
QY 1566 CCGGCGAGCGCGCGCGCGGAGGCGCACTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGT 1625
DB 1379 CCGGCGAGCGCGCGCGGAGGCGCACTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGT 1438
QY 1626 GAGCTGAGAAAGGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1685
DB 1439 GAGCTGAGAAAGGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1498
QY 1686 TCCGAGCCCGGCTTCTCTGTGTGAAAGCCCGCCCTCCGACTGTGAGGCTTCCCGCT 1744
DB 1499 CCGCGCCCAAGTCTTCTCAATGAGGCTGTGCGCCCTGTGCGGAGCTTAAAGAGCTCT 1557

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RESULT 9
US-08-465-982-24
; Sequence 24, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M. J. C. Turner, P. W. Gray,
; APPLICANT: M. J. C. Turner, P. W. Gray,
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release, #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
; US-08-465-982-24

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Query Match 29.5%; Score 718.6; DB 2; Length 2062;  
 Best Local Similarity 69.4%; Pred. No. 3,7e-148;  
 Matches 1123; Conservative 0; Mismatches 404; Indels 92; Gaps 7;

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Qy 148 TGTCCCGCCCGCCCTCAACCTCCCACTCCCGCAAGCCCGGGCTCCATGGCA 207
Db 9 TCTCTATGCCGAGCTCAACCTCAACTCAACCCCAAGCACTTGGAGCTCTGAC 68

Qy 208 TAGCCGAGGACCGGTGTGTCTCACTGTCCGGGGCCGCCATGCCC-CAGCCCTGATGG 266
Db 69 AGACCGAGTCCCGGGAGGCCCGGACACTGCGCTGCCACACTGCTGAGGCCAAATGG 128

Qy 267 GATTTGAGGAGCCACAGCTGCGCCGACATGGGCTTCCCACTGCTGCTGCTGCTG 326
Db 129 GAGGTGAGGAGCCACTACTGTCTGG-CATGGGCTTCTCAACCGGCTGACTGCTGCTG 187

Qy 327 CCACTGTGCTTCCAGCTCTGTTGGCAGATGTGTATCCCGGAGGGGTTTCAGGGGCTGTG 386
Db 188 CCGCTGTGTCTCTGAGCTGTGTGGGAATATACCCCTCAAGGGGTTATTTGGACTGTG 247

Qy 387 CCTCACCCCGGGGAGCTGAGAGAGAGAGAGTCCCTGTCCCAAGGAAATATATACAC 446
Db 248 CTTACCTTAGGGGACAGGAGAGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 307

Qy 447 CCGCAAAATAGCACTTTGTGTGACCAAGTGCCCAAAAGGTACTATCTGTACATGAC 506
Db 308 CTTCAAAATATATGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 367

Qy 507 TGTTCGGGTCCAGGGCCAGAGACCGGACTGACGGGTGTGTGTGTGTGTGTGTGTGTGTGT 566
Db 368 TGTTCAGGGCCGAGGAGATGAGTGTGAGGAGGTGTGAGCGGCTCTTCAACGCT 427

Qy 567 TTGAGAGAACATCTCAGAGATGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 626
Db 428 TCAGAAAACCACTCAGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 487

Qy 627 GTGAGATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 686
Db 488 GTGAGATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 547

Qy 687 TACCGGGAATCTGGGGTGAACCTGGCTTCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 746
Db 548 TACCGGGAATCTGGGGTGAACCTGGCTTCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 607

Qy 747 GGCACAGTGAATATCCCTGCGCAGAGAGAGAGACACATCTGCACTGCAATATGGGC 806
Db 608 GGCACCGTGAATATCCCTGCGCAGAGAGAGAGACACATCTGCACTGCAATATGGGC 667

Qy 807 TTTCTTTCTTAAAGGCGCAAGTGATCTCTGTCTATGATTTGTAAAG--CAAGAGTGC 863
Db 668 TTTCTTTCTTAAAGGCGCAAGTGATCTCTGTCTATGATTTGTAAAG--CAAGAGTGC 727

Qy 864 GAGAGATATGTCCAAACCGGACTTCACTGTGTAAAGCTGTGAGGACCCGAGCACTGA 923
Db 728 ACAGAGTGTGTCTTACCCGAGATGAGATGTAAAGGCACTGAGGACTTCAAGGCACTGA 787

Qy 924 GTACTATTAACCCCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 983
Db 788 GTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 847

Qy 984 TTAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1043
Db 848 TTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907

Qy 1044 ACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1094
Db 908 ACACCTGAAAGAGAGGAGGAGCTTGAAGAACTACTAAGGAGGAGGAGGAGGAGGAGGAGGAG 967

Qy 1095 AACCCACACACACATCTGCTTCACTCAACCCCAAGTTCAGTCTGTCTCAATTC 1154
Db 968 AGCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 1027

Qy 1155 CCTTACATCTCTGTGAGCGGCTCAACTTTCGAG-----CGGTGAGATCTCTCTCC 1205
  
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Db 1028 ACCTTACCTTCAAGCTTCAACCTATATACCCCGGAGCTGTCCCAACTTTGGGCTTCCCGC 1087
Qy 1206 AGCAGACGAGCCCGGCCCATCTTAAAGCTGTGGCCCATCTCCCGGGGCTTCCGGCTTCC 1265
Db 1088 AGAGAGTGTGACACCTTATATAGGGGGCTGTGACCCATCT----- 1128
Qy 1266 ACCCACCCTTGTATCCCGGGGCTTCCGGGCTTCAACCACTCTGTATCCCGGGGCTTCCG 1325
Db 1129 -----TGGACAGGCTTC 1141

Qy 1326 GCTTCCACCCACTCTTCAACCCGAGTTCAAGATGGAGAGCCAGCCCGCCAGGCGCTCC 1385
Db 1142 GCTTCCGAGCCCATCTCCCAACCCCTTCAAGATGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198

Qy 1386 GATCAGCTCGGAGATCCGAGCCCGGAGACCTTACCGGAGTGTGTGACGCGCTGCCCCG 1445
Db 1199 CAGAGCTTGAACACTATATAGACCCCGGAGCGCTGTATACCGCTGTGTGTGTGTGTGTGTGT 1258

Qy 1446 TCGCGCTGAAAGAGTTGTGTGCGGCGGCTGTGAGACTAGCAGACAGAGATCGAGCGCTG 1505
Db 1259 TTGCGCTGAAAGAGATTCGTGCGGCGCTGTAGGCTGTAGCAGACAGAGATCGATCGGCTG 1318

Qy 1506 GACTGTGAAAGAGCGGCGCCACCTGCGGAGAGCCGACATGACATGCTGTGGCGGCTGCGG 1565
Db 1319 GACTGTGAAAGAGCGGCGCTGCGGAGAGCGCAATACGATGCTGTGGAGCTGTGAGG 1378

Qy 1566 CCGGCGACGCGCGGCGCGGAGGAGCAAGCTGTGAGCTGTGGGCGCGCTGTCAAGGAGATG 1625
Db 1379 CCGGCGACGCGCGGCGCGGAGGAGCAAGCTGTGAGCTGTGGAGCGGCTGTCCGAGATG 1438

Qy 1626 GACTGTGTGGGTTTCCGTGAAAGAGATGAGAGAGCGCTGTGGTGTGCGCGCGCTTCCG 1685
Db 1439 GACTGTGTGGGTTTCCGTGAGAGAGATGAGAGAGCGCTTGTGCGGCGCGCGCTTCCG 1498

Qy 1686 TCCGAGCGCGCGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1744
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RESULT 10
US-08-406-824A-3
; Sequence 3, Application US/08406824A
; Patent No. 6541610
; GENERAL INFORMATION:
; APPLICANT: SMITH, Craig A.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
; FILE REFERENCE: A-71592
; CURRENT APPLICATION NUMBER: US/08/406,824A
; PRIOR FILING DATE: 1995-03-20
; PRIOR APPLICATION NUMBER: US 08/255,849
; PRIOR FILING DATE: 1994-06-08
; PRIOR APPLICATION NUMBER: US 07/860,710
; PRIOR FILING DATE: 1992-03-30
; PRIOR APPLICATION NUMBER: US 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: US 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: US 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: US 07/403,241
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
; OTHER INFORMATION:
; FEATURE:
  
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Db 1174 CTGACAGGAGTGTGAGAGGGGCTCTTCACCGCTTCAGAAAAACACCTCAGACACTGCCT 1233
Qy 593 GAGCTGCTCCAGGTCCGGAGCGAAATGTTCCAGGTGAGATTTCGCTTGTGTAGTGA 652
Db 1234 CAGCTGCTCCAAATGCGAAAGGAATGGTCAAGTGAATCTCTTTCGACAGTGA 1293
Qy 653 CCGGACACTGTGTGCGGCTGCGAGAAACAGTACCGGGAATCTGGGGTGAAGTGG 712
Db 1294 CCGGACACCGTGTGTGCTGCGAGAAACAGTACCGGCAATTGAGTGAAGAACT 1353
Qy 713 CTTCCGCTGTGAAGCTGAGCCTCTGTCCAAATGCGACAGTGAATATCCCTGCGAGGA 772
Db 1354 TTTCAGTGTCTTCAATTGACAGCCTCTGCTCAATGGGACCGTGCACTCTCTGCGAGGA 1413
Qy 773 GAGACAGACACCATCTGCGCATATGGCTTCTTTAAAGGCGCCAGTGCAT 832
Db 1414 GAAACAGAACCGTGTGCACTGCGCATGCAAGTTCCTTCTAAGAGAAACGAGTGTGT 1473
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Db 1534 GAATGTAAAGGCACTGAGGACTCAGGCACACAG 1568
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Search completed: September 15, 2003, 07:52:08  
Job time : 139 secs





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QY 121 GGGTTTGAAGTCTCTCCGGATTGGGCTGTGTCCCGCCCCAGTCTCAACCTTCACTCCCC 180
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QY 181 GACCCGAGGCCCCGGGCTTCACTGGGCATACGAGAGACCGTGTGCTGTCACTGTCCGG 240
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QY 241 GCGCCGACTGCGCCGAGCCCTGATGGGGGATTGAGAGGCGACAGCTGGCCGACATGGGCC 300
DB 241 GCGCCGACTGCGCCGAGCCCTGATGGGGGATTGAGAGGCGACAGCTGGCCGACATGGGCC 300
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DB 301 TCCCCACCGTCTGGCCTGTGCTGTGCACTGTGTCTTCAAGCTTGTGTGGCAAGTGT 360
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DB 361 ACCCCGAGGGGTTTCAGGGGCTGTGTCTTCAACCCCGGGGACCTGGAGAGAGAGAGTTC 420
QY 421 CCTGTCCCGCAAGAAATATACACCCCGCAAAATAGACCAATTTGCTGTCAACAAATGCC 480
DB 421 CCTGTCCCGCAAGAAATATACACCCCGCAAAATAGACCAATTTGCTGTCAACAAATGCC 480
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DB 841 ATGATTTGTAAGAACAAAGAGTGGAGAGATTATGTCCAAACCGCATCTTCAACTGGTAAAG 900
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DB 1081 CGGCGCCAGGCTTCAACCCGACCAACCATCTGTCAAGCTTCAACCCGAAAGTTCCAGTCC 1140
QY 1141 CTGTCTCATTTCCCTTTACATCTCTGTGACCGGTCGAATTGAGAGCCGTCCGATCTTC 1200
DB 1141 CTGTCTCATTTCCCTTTACATCTCTGTGACCGGTCGAATTGAGAGCCGTCCGATCTTC 1200
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DB 1381 CCCCCGATCAGCTGCGGATGCGAGCCCGGACCCCTGTATGACGGGTGTGAGACGGCGTGC 1440
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DB 1801 TGTGAGACTCTCTGTTTTGTTTTGTTTTTCTGGAGAGAGAGTTCTGGAGAGAGAGAG 1860
QY 1861 GATCTGGAGCACTGACCTGTGTCTGTACTCACTAGAGTACATGCTTTTCTCAGCTGCC 1920
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DB 1921 TGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
QY 1981 TGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
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DB 2101 GAGAACTCAGCAAGGCACTTGGGAACTTACGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
QY 2161 ATTAAGCCATCTTTGTATTCACCTGTGCACTTCATTCATTCATCTGTATACATAATAGAA 2220
DB 2161 ATTAAGCCATCTTTGTATTCACCTGTGCACTTCATTCATTCATCTGTATACATAATAGAA 2220
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DB 2221 CTTTGTGTGCGCTGTGGAACAGCTGAACTGTCCCGAGGAGCGGGGAGAGAGAGAGAA 2280
QY 2281 TGGGGCTTCCCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
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2881	TTG3G6CCCTCCCAAGG3AGCTGACGTTCAGTTTCAGTTCAGTCGCTCACTCGCTGCCACT	2341	CTTTGGCGACCCCTGTGGAATCGCAGGGACCTCTGTGTAATACATCAAAAATCTTCCAAATTAAAG	2401	CTTCGCCCCTGGAGGACCTGTGTTAAAAAAAAAAAAAAAAAAAA
		2341	CTTTGGCGACCCCTGTGGAATCGCAGGGACCTCTGTGTAATACATCAAAAATCTTCCAAATTAAAG	2401	CTTCGCCCCTGGAGGACCTGTGTTAAAAAAAAAAAAAAAAAAAA
		2401	CTTCGCCCCTGGAGGACCTGTGTTAAAAAAAAAAAAAAAAAAAA	2440	CTTCGCCCCTGGAGGACCTGTGTTAAAAAAAAAAAAAAAAAAAA

RESULT 2  
US-09-899-422-16  
Sequence 16 Application US/09899422

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1 Patent No. US200602090676A1
2 GENERAL INFORMATION:
3 APPLICANT: Hauptmann, Rudolph
4 APPLICANT: Himmeler, Adolph
5 APPLICANT: Maurer-Foggy, Ingrid
6 APPLICANT: Stralowa, Christian
7 TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
8 TITLE OF INVENTION: Them
9 FILE REFERENCE: 98,385-H
10 CURRENT APPLICATION NUMBER: US/09/899,422
11 CURRENT FILING DATE: 2001-08-21
12 PRIOR APPLICATION NUMBER: 09/525,998
13 PRIOR FILING DATE: 2000-03-15
14 PRIOR APPLICATION NUMBER: 08/483,676
15 PRIOR FILING DATE: 1995-02-01
16 PRIOR APPLICATION NUMBER: 08/153,287
17 PRIOR FILING DATE: 1993-11-17
18 PRIOR APPLICATION NUMBER: 07/821,750
19 PRIOR FILING DATE: 1992-01-02
20 PRIOR APPLICATION NUMBER: 07/511,430
21 PRIOR FILING DATE: 1990-04-20
22 NUMBER OF SEQ ID NOS: 87
23 SOFTWARE: PatentIn Ver. 2.0
24 SEQ ID NO 16
25 LENGTH: 2141
26 TYPE: DNA
27 ORGANISM: Artificial Sequence
28 FEATURE:
29 NAME/KEY: CDS
30 LOCATION: (213)..(1580)
31 OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
32 US-09-899-422-16

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Query Match	Score	DB	Length
30.2%	737	9	2141

Matches 1152; Conservative 1; Mismatches 401; Indels 95; Gaps 8;

QY	101	GGGCCGAGGGCTGGGCTTCCGGGTTGAGTCTCCGATTGGGCTGTC--TCCCGCC	157
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QY	158	CCAGTCTCAACCCCTCACTCCCGACCCGAGGCCCGGGCTCCACTGGGCATACGGAGGA	217
Db	77	CGAGTCTCAACCCCTCAACTGTCAACCCCAAGGACATTGGGACGTCCTGGACACAGCCAGTGC	136
QY	218	CCGCTTTCGTGCACTGTCGCGGGGCGGCACCTGCCCCAGCCCTATGGGGGATTGAGG	276
Db	137	CCGGGAGGCCCAAGCACTGCGCCTGTCCACACTGCTGAGCCCAATGGGGGATGAGAG	196
QY	277	GCACAGCTGGCCGAGCATGGGCTTCCCAACCGCTGAGCTGTGCTGTCCACTGGTGC	336
Db	197	GCATATGCTGTGTGG-CATGGGCTCTCCACCGTGTCACTGACTGTGCTGCCACTGGTGC	255
QY	337	TTCACAGCTGTGTGGCAGATGTGTAAACCCGACGGGGTTCAAGGGGCTGATCCCTCAACCCG	396
Db	256	TCTGTAGAGCTGTGTGGGGAATATTAACCCCTCAGGGTTATTGGACTGTGCTCCTCACTAG	315
QY	397	GGGACCTGGAGAAAGAGAGAGTCCCTGTCTCCCAAGAAAATATTAACACCCGCAATA	456

D	b	316	GGGACAGGGAGAGAGAGATAGTGTGTGTCCCCAGGAAATATATCATCCCTCAAAATA	375
O	y	457	GCACCAATTGGTGCACCAAGTGCACAAAGTACTTCTGTACATAGACTGTCCGGTCC	516
D	b	376	ATTGGAATTGTCTTACCAAGTGCACAAAGAACCTTCTGTACAAATGACTGTCCAGGCC	435
O	y	517	CAAGGCGCAGACACGGAATGACAGAGGTGTGTGCCCTGACCTTACATGCGCTGGAGAAC	576
D	b	436	CGGGCAGAGATAACGACTGCAGAGGAGTGTAGAGACGGCTCTCTTACACGCTTCAGAAAAC	495
O	y	577	ATTCTCAGACGATGCTGAGCTGCTCCAGAGTGC CGGAGCGAAATTTCCAGGTGAGATT	636
D	b	496	ACCTCAGACGACTGCTCAGCTCTCCAAATGCCAAAGAAATGGTCCAGTGGAGATCT	555
O	y	637	CGCCTTGTGTAGTGAACCGGAGACATGTGTGCGGCTGCAGAGAGAACCAAGTACCGGAAT	696
D	b	556	CTTCTTGCAAGTGGACCGGGACACCGTGTGTGCTCAGAGAGAACAGTACCGGAT	615
O	y	697	ACTGGGGTGAACCTGGCTTCCGGTGTCTGAACCTGCACACCTCTGTGCCAATGACACATGA	756
D	b	616	ATTGAGAGAAAACCTTTTCCAGTCTTCAATTCAGCTCTGTGCTTCAATGAGACCGTGC	675
O	y	757	ATTATCCCTGSCAGAGAGACAGACACATCTGCCACTGCAATATGGCTTCTTTCTTA	816
D	b	676	ACCTCTCTGTCGAGAGAAACAGAACACCGTGTGCACCTGCAATGACAGTTTCTTTCTAA	735
O	y	817	AAGCGGCCAATGTCATCTCTGTCAATGATTGTAA--CAAGAGTGCAGAGATTAT	873
D	b	736	GAGAAAACGAGTGTCTCTGTAGTAACTGTAGAAAAGCTGAGAGTGCACGAAGTGT	795
O	y	874	GTCCAACCCGACCTTCAACTGTGTAAAGCTCAGAGACCGAGGACATACACTATTAAC	933
D	b	796	GCTCAACCCAGATTGAGAAATGTAAAGGCACTGAGAGACTCAGGACCAACAGTGTCTGTGC	855
O	y	934	CCCTGATGATTGTCTTCCGGCTTTAGCCTGCGATCTTTCGCTCTGTGCTGTACATATGC	993
D	b	856	CCCTGGTCAATTTCTTGTGTCTTTGCTTTTATCCCTCTCTTCAATGGTTAAATGATAC	915
O	y	994	GCTACACAGCGGTGAAAGCCCAAGCTCTAATCCATCATTTGCGGCGAGTGCATCTGTGTA	1053
D	b	916	GCTAACAAACGGTGGAAAGTCCAAAGCTTCACTCAATGTTTGTGGGAAATGCAACCTGAA	975
O	y	1054	AAGAGGGGAGCAGAA-----CTCTGTGTCCGGGCCCCAGGCTTCAACCCACCA	1104
D	b	976	AAGAGGGGAGCCTTGAAGGAATCTAATAGCCCTCGGCCCCAAACCCAAAGCTTCAAGTC	1039
O	y	1105	CCACCATGTGTTACAGCTCCACCCCAAGTCCAGTCCGTCCATTCGCCCTTACAATCT	1164
D	b	1036	CCACTCCAGCTTACACCCCAACCTCGGCTTCAGTCCGTGCCAGTTCACACTTCACT	1099
O	y	1165	CCTGTGACCGGTCCAACTTTCGAG-----CCGTGCATCTTCCCTCCAGCAGACGG	1215
D	b	1096	CCAGCTCAACTAATACCCCGGTGACGTGCCAATTTGCGGCTGCCCGCAGAGAGGTGG	1155
O	y	1216	CCCGGCCCATCTAAAGGTGAGCCCATCTCTCCGAGGCTTCCGAGCTTCCACCACTCT	1275
D	b	1156	CACCAACCTTATCAGGGGGCTGACCCCACTCT-----	1186
O	y	1276	GTAACCCGGGGCTTCGGGCTTCCACCACTCTGTACCCCGGGGCTTCCGGCTTCCACC	1339
D	b	1187	-----TGCCACAGCTTCCCTCTCCAGC	1209
O	y	1336	ACCTTGCACCCCAAGTTCAAGAGTGGAAAGCCAGGCGCCCGAGGCGCCCGCATGACTCG	1399
D	b	1210	CCATCCCAACCCCTTCAAGAGTGGAGACAGCGCCACA---AGCACAGAGCTTAG	1266
O	y	1396	CGGATGCAGACCCCGCGACCTGTACCGGCTGTGAGACGCGCTGCCCCGTGCGCTGGA	1455
D	b	1267	ACACTGATGACCCCGCGACGCTGTACGCGTGTGTGGAAAGATGTGCCCCGTGTGGCTGGA	1326
O	y	1456	AGGATTTGTGTCCGCGCTTGGGACTGAGACGAGACGATATGAGCGGTGAGGCTGAGA	1515

Db 1327 AGGAATTCGTGGCGGCGCTAGGAGTGAAGGACCAAGATGATGCGGTGAGCTGCAGA 1386  
 Oy 1516 AGGGGGGACCACTGGCGGAGGGGAGGTATAGATGCTGGCGGCTGGCGGCGGACAGC 1575  
 Db 1387 AGGGGGGCTGCTGGCGGAGGGGAGGTATAGATGCTGGCGGCTGGAGGCGGCGACAGC 1446  
 Oy 1576 CGCGCGCGAGGCGCAAGCTGAGTGTGGGCGGCGCTGCTCAAGGACATGAGACTGTGG 1635  
 Db 1447 CGCGGCGGAGGCGCAAGCTGAGTGTGGGAGCGGTGCTCGGCGACATGAGACTGTGG 1506  
 Oy 1636 GTTGGCTGAAAAATATAGAGAGGCGCTGGGCGGCGGCGCTCGGCTCGGAGAGCC 1695  
 Db 1507 GCTGGCTGAGAGCATCGAGAGGCGCTTGGCGGCGGCGGCGCTCGGCGGCGGCGCA 1566  
 Oy 1696 GCCTTCTGTGTGAAGCGCGGCGGCTCGG 1724  
 Db 1567 GTCTTCTGATGAGGCTGCGGCGCTGCG 1595

RESULT 3  
 US-09-898-234-16  
 ; Sequence 16, Application US/09898234  
 ; Patent No. US2002015112A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hauptmann, Rudolph  
 ; APPLICANT: Hummel, Adolph  
 ; APPLICANT: Maurer-Fogd, Ingrid  
 ; APPLICANT: Stralowa, Christian  
 ; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
 ; FILE REFERENCE: 98,385-1  
 ; CURRENT APPLICATION NUMBER: US/09/898,234  
 ; CURRENT FILING DATE: 2001-07-03  
 ; PRIOR APPLICATION NUMBER: 09/525,998  
 ; PRIOR FILING DATE: 2000-03-15  
 ; PRIOR APPLICATION NUMBER: 08/383,676  
 ; PRIOR FILING DATE: 1995-02-01  
 ; PRIOR APPLICATION NUMBER: 08/153,287  
 ; PRIOR FILING DATE: 1993-11-17  
 ; PRIOR APPLICATION NUMBER: 07/821,750  
 ; PRIOR FILING DATE: 1992-01-02  
 ; PRIOR APPLICATION NUMBER: 07/511,430  
 ; PRIOR FILING DATE: 1990-04-20  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 16  
 ; LENGTH: 2141  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (213)..(1580)  
 ; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in  
 ; OTHER INFORMATION: LINF-R2  
 US-09-898-234-16

Query Match 30.2%; Score 737; DB 10; Length 2141;  
 Best Local Similarity 69.9%; Pred. No. 8.2e-177;  
 Matches 1152; Conservative 1; Mismatches 401; Indels 95; Gaps 8;

Oy 101 GCGCGAGGCGGCTGCGGCGGCTTGAAGTCTCCGATGGGCTGTG---TCCCGCC 157  
 Db 17 GCGTTCAGATTCTGGCTTGGGCTTCAAGATCACTGGAGCAAGGCGCGTGAATCTATGCC 76  
 Oy 158 CCAAGTCAACCTTCACCTCCCGAGCGGAGCGGCGGCTCACTGGGAGATACCGAGGA 217  
 Db 77 CGAGTTCACCTTCACCTTCACCTCCCGAGCGGAGCGGCTCACTGGGAGATACCGAGATC 136  
 Oy 218 CCGTGTGCTGTCACTGTGCGGCGGCGGCACTGCCCC-AGCCCTGATGGGAGATTGAGG 276  
 Db 137 CCGGAGAGCCCGAGCACTGCGCGGCGGCACTGCCCTTGAAGCCAKATGGGGAATGAGAG 196  
 Oy 277 GCCACAGCTGCGCGAGCATGGGCTCCCGACCGTGCCTGCTGCTGCACCTGTGCTG 336

Db 197 GCGATAGCTGTGTGG-CAATGGGCTCTTCACCGGCTGCTGAGCTGTGTCACATGCTGC 255  
 Oy 337 TTCCAGCTCTGTGGCAGATGTGATACCCCGAGGGGTTTCAAGGGCTGTGCTCCACCCCG 396  
 Db 256 TCTGTGAGCTGTGTGGTGAATATATACCCCTCAGGGGTTATTTGATGTGTCTCCCTCAG 315  
 Oy 397 GGGACCTGGAAGAAGAGAGTCCCTGTCCCCAAGAAATATATACCACTCCGAAATA 456  
 Db 316 GGGACAGGAGAGAGAGATGTGTGTCCCAAGAAATATATATATATATATATATATATAT 375  
 Oy 457 GCACATTTGTGTGACCAAGTGCACCAAGGTACTATCTGTAGAAATGACTGTGCGGGCT 516  
 Db 376 ATTTGATTTGTGTATACCAAGTGCACCAAGGTACTATCTGTAGAAATGACTGTGCGGG 435  
 Oy 517 CAGGCGAGACACGAGCTGACAGGCTGTGTGCGGCGGCGGCTTCACTGAGGAGAAC 576  
 Db 436 CCGGCGAGGATACGAGCTGACAGGAGTGTGAGAGCGGCTCCTTCAAGGCTTCAAGAAAC 495  
 Oy 577 ATCTCAGAGATGCTGAGCTGCTCAAGTGTGCGGCGGAGCAAAATGTCAGGTGAGATTT 636  
 Db 496 ACTCAGACACTGCTCAGCTGTCCAAATGCGAAAGAAATGTTAGGTGAGATCT 555  
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 Oy 934 CCTGTGATGATTTCTTGGGCTTGTGCTGAGCTTGTGCTGTGCTGTGATGATGTC 993  
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 Db 916 GCTACCAAGGCTGAGATGCAAGCTTCACTGATTTGTTGAGGAATGCAACACTGAA 975  
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 Db 976 AAGAGGGGGAGCTTGAAGAACTACTAATGAGGCTTGGGCGGCGGCAAGCTTCAAGTC 1035  
 Oy 1105 CCAACATCTGCTTCACTGACACCGCAAGTTCAGTGTGTCTCATCTCCCTTACATCT 1164  
 Db 1036 CCACTCAGGCTTCACTGACACCGCAAGTTCAGTGTGTGTGCTGCTGCTGCTGCTGCT 1095  
 Oy 1165 CTTGTGACCGGCTCACTTGTGAG-----CGTGTGATCTCTCTGAGGAGAGCG 1215  
 Db 1096 CCAAGCTCACTTATACCCCGGTAAGTGTGCACTTGTGCGGCTCCCGGAGAGAGGTGG 1155  
 Oy 1216 CCGCGGCGGCTTAAAGGCTGTGCGGCTTCTCCCGGGGCTCCGGGCTCAACCACTCT 1275  
 Db 1156 CACCACTTATCAGGGGCTGACCCCACTCT----- 1186  
 Oy 1276 GTACCCCGGGGCTTCCGGCTTCAACCACTTGTATCCCGGGGCTTCCGGCTTCAACCC 1335  
 Db 1187 -----TGGAGACAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1209  
 Oy 1336 ACCTTGACCCCAAGTTCAAGATGGAGAGCAGGCGGCGGCGGCGGCTGCTGCTGCTGCTG 1395

Db 1210 CCATCCCCAACCCCTTCAGAAAGTGGAGAGACAGCCCAACA---AGCCAGAGAGCTTAG 1266  
Qy 1396 CGAGTCCGACCCCGCGACCCCTGTACGCGGTGTGAGAGCGCGTCCCGCGCTGCGCTGGA 1455  
Db 1267 ACACTGATGACCCCGCGACCGCTGTACCGCGGTGTGAGAGAGAGTCCCGCGCTGCGCTGGA 1326  
Qy 1456 AGAGATTGTCGGCGCGCTGAGACTGAGCCGACAGATGAGAGCTGGAAGTGTGAGAG 1515  
Db 1327 AGGAATTCGTGCGCGCTGTAGGCGTGAAGCAGCAGAGATGATCGGTGAGCTGACGA 1386  
Qy 1516 ACCGCGCCGACCTGCGAGAGCGGACGTACAGCATCTGACGCGCTGCGCGCGCGACGCG 1575  
Db 1387 ACCGCGCGCTGCTGCGAGAGCGGACATACAGCATCTGACGCGCTGAGAGCGCGACGCG 1446  
Qy 1576 CGCGCGCGAGAGCGGACGTGAGCTGTGCGCGCGCTGCTGACGAGACATGAGACTGTGCG 1635  
Db 1447 CGCGCGCGAGAGCGGACGTGAGCTGTGCGCGCGCTGCTGACGAGACATGAGACTGTGCG 1506  
Qy 1636 GTTCCCTGGAAGAAATAGAGAGAGCGCTGAGGTGCGCGCGCGCTGCGCTGCGAGCGCG 1695  
Db 1507 GCTGCGCGAGAGAGCATGAGAGAGCGCTTGTGCGCGCGCGCGCGCTGCGCGCGCGCGCA 1566  
Qy 1696 GCCTTCTGTGTAAGCGCGCGCGCTGCG 1724  
Db 1567 GTCTTCTGATGAGGCTGCGCGCGCTGCG 1595

## RESULT 4

US-09-999-429A-26  
Sequence 26: Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummel, Adolph  
APPLICANT: Mauser-Fogy, Ingrid  
APPLICANT: Stralowa, Christian  
TITLE OR INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 26  
LENGTH: 2141  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in  
NAME/KEY: CDS  
LOCATION: (213)..(1577)  
US-09-999-429A-26

Query Match 30.2%; Score 737, DB 10; Length 2141;  
Best Local Similarity 69.9%; Pred. No. 8.2e-177;  
Matches 1152; Conservative 1; Mismatches 401; Indels 95; Gaps 8;

Qy 101 GGCGGAGAGGCGCTTCCGAGTTTGAAGTCTCCGATTTGGGCTGCG---TCCCGCGC 157  
Db 17 GGCTCCAGTTTGGGCTTGGGGTTCAAGATCACTGGGACCAAGGCGGTGATCTTATGCC 76

Qy 158 CCACTCTCAACCTCTCACTCCCGAGCCCGAGCCCGGCTTCACTGGGCAATACCGAGGA 217  
Db 77 CGAGTCTCAACCTCTCACTGTCACACCGAGGCACTTGGAGAGTCTCGGACAGACCGAGTC 136  
Qy 218 CCGTGTGCTGTCACTGTCCGCGGCGCGCACTGCGCC-AGCCCTGATGGGGATTTGAGAG 276  
Db 137 CCGGAGAGCCCGAGCACTGCGCGTGCACACTGCGCTGAGCGCCAKATGGGGAGTGAAG 196  
Qy 277 GCGACAGTGGCGCGGACATGGGCGCTCCCGACCGGCGCTGCGCTGCTGCTGCTGCTGCTG 336  
Db 197 GCGATAGCTGTCTGCG-CATGGGCTTCTCACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 255  
Qy 337 TTCCAGCTCTGTTGGCAGATGTGTACCCCGAGGGGTTCAAGGGGCTGCTGCTGCTGCTG 396  
Db 256 TCTGAGAGCTGTGTGTGGAATATACCTCTCAGGGGTTATTTGAGCTGTGCTGCTGCTGCTG 315  
Qy 397 GGGACCTGAGAGAGAGAGAGAGTCCCTGTCCAGAGAAATATATACCGCGGAAATA 456  
Db 316 GGGACAGGGAGAGAGAGAGATGTGTGTGTCCCAAGGAAATATATATACCTGCAATA 375  
Qy 457 GCACCAATTTGTGCGACCAAGTGCACAAAGGTACTATCTGTATCAATGACTGTGCGGGT 516  
Db 376 ATTGATTTGTGTGTACCAAGTGCACAAAGGAACTTGTATCAATGACTGTGCTGCTGCTG 435  
Qy 517 CAGGGCGAGACACGAGCTGAGAGGTGTGTGCGCGCTGCGACCTGACCTGCTGCTGCTGCTG 576  
Db 436 CGGGGAGAGATGAGGACTGAGAGAGGTGTGTGAGAGCGGCTCTTCAACGCGCTTCAAGAAAC 495  
Qy 577 ATCTCAAGCATGCTGAGCTGTCTGAGAGGTGTGTGCGGGAGCAAAATTTCCAGGTGAGATT 636  
Db 496 ACCTCAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 555  
Qy 637 GCGCTGT 696  
Db 556 CTTTCTTCAAGT 615  
Qy 697 ACTGGGTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756  
Db 616 ATTGAGTGAAGAACTTTTCAAGT 675  
Qy 757 ATATCCCTGCGAGAGAGAGAGAGACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816  
Db 676 ACCTCTCTGCGAG 735  
Qy 817 AAGGCGCAAGT 873  
Db 736 GAGAAAGAGAGT 795  
Qy 874 GTCCACCCGAGCTTCAAGT 933  
Db 796 GCGTACCCGAGT 855  
Qy 934 CCGT 993  
Db 856 CCGT 915  
Qy 994 GTTACAGCGGT 1053  
Db 916 GTTACAGCGGT 975  
Qy 1054 AAGAGGGGAG 1104  
Db 976 AAGAGGGGAG 1035  
Qy 1105 CCACCATGT 1164  
Db 1036 CCACTTCAAGCTTCAACCCGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1095  
Qy 1165 CCGT 1215  
Db 1096 CCACTTCAAGCTTCAACCCGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1155

QY 1216 CCCCCCATCTMAAGGCTGAGCCCCCATCTCCCGGGGCTCCCGGCTCAACCCACTCT 1275  
 DB 1156 CACCACCTTATCAGAGGGGCTGACCCCATCT----- 1186  
 QY 1276 GTACCCCCGGGGCTCCGGGCTCAACCCACTCTGTAACCCGGGGCTCCGGGCTCCACC 1335  
 DB 1187 -----TGGCAGACCTCGGCTCCGAC 1209  
 QY 1336 ACCCTGCAACCCCACTTCAAGAGTGGAGACCAAGGCCCCCAAGCCCCCAATCAAGCTCG 1395  
 DB 1210 CCATCCCAACCCCTTCAAGAGTGGAGACAGGCCCCACA--AGCCAGAGAGCTTAG 1266  
 QY 1396 CGAGTGCAGACCCCGCAGACCTGTACGCGGTGTGAGAGCGGTGCCCCCTCGCGCTGGA 1455  
 DB 1267 AACTGATGACACCCCGCAGACCTGTACGCGGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1326  
 QY 1456 AGGAGTGTGTGCGGCGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1515  
 DB 1327 AGGAGTGTGTGCGGCGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1386  
 QY 1516 ACGGCGCGCACCTGCGCGAGCGAGTACAGATGCTGGCGGCTGGCGGGCGCGCACGC 1575  
 DB 1387 ACGGCGCGGTGCTGCGCGAGCGAGTACAGATGCTGGCGGCTGGCGGGCGCGCACGC 1446  
 QY 1576 CGCGCGCGGAGGAGCAGCTGAGAGTGTGAGGCGCGGCTGAGAGAGATGAGAGCTGTGG 1635  
 DB 1447 CGCGCGCGGAGGAGCAGCTGAGAGTGTGAGGCGCGGCTGAGAGAGATGAGAGCTGTGG 1506  
 QY 1636 GTTCCCTGGAACATAGAGAGAGGCGCTGAGGCGCGGCTGAGAGAGATGAGAGAGAGAG 1695  
 DB 1507 GCTCCCTGAGAGATCAGAGAGAGGCGCTTGTGCGGCGCGGCTGAGAGAGAGAGAGAG 1566  
 QY 1696 GCCTTCTGTGGAAGCGCGGCGGCTGCG 1724  
 DB 1567 GTCTTCTGATGAGGCTGCGGCGGCTGCG 1595

# RESULT 5

US-09-792-356-16  
 Sequence 16, Application US/09792356  
 Publication No. US20020183485A1  
 GENERAL INFORMATION:  
 APPLICANT: Hauptmann, Rudolph  
 APPLICANT: Himmler, Adolph  
 APPLICANT: Maurer-Fogy, Ingrid  
 APPLICANT: Stralow, Christian  
 TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
 FILE REFERENCE: 98,385-G  
 CURRENT APPLICATION NUMBER: US/09/792,356  
 PRIOR FILING DATE: 2001-08-17  
 PRIOR APPLICATION NUMBER: 08/477,639  
 PRIOR FILING DATE: 1995-06-07  
 PRIOR APPLICATION NUMBER: 08/383,676  
 PRIOR FILING DATE: 1995-02-01  
 PRIOR APPLICATION NUMBER: 08/153,287  
 PRIOR FILING DATE: 1993-11-17  
 PRIOR APPLICATION NUMBER: 07/821,750  
 PRIOR FILING DATE: 1992-01-02  
 PRIOR APPLICATION NUMBER: 07/511,430  
 NUMBER OF SEQ ID NOS: 87  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 16  
 LENGTH: 2141  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (213)..(1580)  
 OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in  
 OTHER INFORMATION: TNF-R2  
 US-09-792-356-16

Query Match 30.24; Score 737; DB 10; Length 2141;  
 Best Local Similarity 69.94; Pred. No. 8.2e-177;  
 Matches 1152; Conservative 1; Mismatches 401; Indels 95; Gaps 8;

QY 101 GGGCGAGGGCTGAGCTTCCGGGTTGAGGTCTCCGATGAGGCTGTG--TCCCGCC 157  
 DB 17 GGTCTCAGTTCTGGACCTTTGGGTTCAAGATCATCGGAGACAGGCGGTGATCTGATGCC 76  
 QY 158 CCAAGTCAACCTTCCACTCCCCCAAGAGCCCGGCTCCACTGAGGATACCGAGAGA 217  
 DB 77 CGAGTCTCAACCTTCAACTGTCAACCCAGGACCTTGGAGAGTCTTGACAGACCGAGTTC 136  
 QY 218 CCGTGTGCTGCACTGTGCGGGCGGCACTGCCCC-AGCCCTGATGGGGATTGAGAG 276  
 DB 137 CCGGAGAGCCCAAGACTGCTCCGTCACACTGCTGAGCCCTGAGCCCAATGGGGAGTGAAG 196  
 QY 277 GCGACAGCTGACCGGACATGAGGCTCCCAACCGTGCCTGCTGCTGCTGCACTGTGTC 336  
 DB 197 GCGATAGCTGTCTGG-CATGGGCTTCCACCGTGCCTGAGCTGTGCTGCACTGTGTC 255  
 QY 337 TTCCAGCTCTGTGACAGATGTGTACCCCGAGGGGTTCAAGGGCTGTCTCAACCCCG 396  
 DB 256 TCTGAGAGCTGTGTGAGAAATATACCCCTCAGGGGTTATGAGACTGTGCTCTCACTAG 315  
 QY 397 GGGACCTGAGAGAGAGAGAGAGTCCCTGTCCCAAGGAAATATACCAACCGGAAATA 456  
 DB 316 GGAAGAGGAGAGAGAGAGATATGTGTGTCCCAAGGAAATATATCACTCTCAAAATA 375  
 QY 457 GCACCATTTGTGACCAAGTGCACCAAGGATACCTATCTGTACAAATGACTGTCCGGTTC 516  
 DB 376 ATTGATTTGTCTGTACCAAGTGCACCAAGGATACCTATCTGTACAAATGACTGTCCAGGC 435  
 QY 517 CAGGGCGAGACAGGACTGCAAGGTTGTGCTCCCTGCACTTACATGCTTTGAGAGACC 576  
 DB 436 CGGGCAGGATACGAGACTGCAAGGTTGTGAGAGCGGCTCTTCAACGCTTCAGAGAAACC 495  
 QY 577 ATCTCAGAGATGCTGAGCTGCTCCAGAGTCCGGGAGCAAAATGTTCCAGGTGAGATTT 636  
 DB 496 ACTCTCAGACTGCTCTCAGCTGCTCCAAATGCTCCAAAGGAAATGAGTCAAGTGAATCT 555  
 QY 637 CGCCTTGTGATGAGACCGGAGCACTGTGTGCGGCTGCAAGAGAAACGATACCGGAAAT 696  
 DB 556 CTTCTTGACAGTGAACCGGAGCACCGTGTGTGCTGCAAGAGAAACGATACCGGAAAT 615  
 QY 697 ACTGGGTGAAACTGCTTCCGCTGTCTGAACCTGAGCTGTGCTCCCAATGAGCAAGTGA 756  
 DB 616 ATTGAGAGAAACCTTTTCCAGTCTTCAATTCAGCTCTGCTCAATGAGGACCGTGC 675  
 QY 757 ATATCCCTGCGCAGAGAGAGACAGACCAATCTGCCACTGCTCATATGAGGCTTTCTTTCTTA 816  
 DB 676 ACTCTCTCTGCGAGAGAGAGAGAGAGACCGTGTGACTGCTGCAAGGATTTCTTTCTTA 735  
 QY 817 AAGCGCCCAAGTGCATCTCTGTGATGATGTAAGAA--CAAGAGTGCAGAAATTAT 873  
 DB 736 GAGAAACAGAGTGTCTCTGTGATGATGTAAGAAAGCGCTGAGTGCAGAAATTAT 795  
 QY 874 GTCAACCCCACTTCAACTGTGTAAGACTGCAAGCCCGAGGACATACATATAC 933  
 DB 796 GCGTACCCCAAGTGAAGATGTAAGGCACTGAGACTGAGGACCACTACATGCTGTTC 855  
 QY 934 CCTGTGATTTGTCTTGGGCTTGGCTGAGCATCTTGCCTGTGCTGTGCTTACATATGC 993  
 DB 856 CCTGTGATTTGTCTTGGGCTTGGCTTGTATATCCCTCTCTTCAATGTTAATGATTC 915  
 QY 994 GCTACCAAGCGGTGAGAGCCCAAGCTTACTCATCTTGTGAGGAGTGCAGCTGTGTA 1053  
 DB 916 GCTACCAAGCGGTGAGAGCTTACTCATCTTGTGAGGAAATGCAACCTGTA 975  
 QY 1054 AAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1104  
 DB 976 AAGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1035

Query	Subject	Score	DB	Length	2175;
148	TGTCCCGCCGAGCTCAACCTCTCACTCCCGACCCGAGGCCCCGAGCTCACTGGCA	29.8*	DB 13;	Length 2175;	
110	TCTCTATGCCGAGCTCAACCTCTCACTCCCGACCCGAGCACTTGGACGCTCGAC	29.8*	DB 13;	Length 2175;	
208	TACGAGGAGCCGTGTGTCTCACTGTGCGGGCCGCACTGCC-C-CAGCCCTGATGGG	29.8*	DB 13;	Length 2175;	
170	AGACCCAGTCCCGGAGAGCCCGACAGCTGCGCTGCACACTGCGCTGAGCCCAATGGG	29.8*	DB 13;	Length 2175;	
267	GGATTGAGAGGCGACAGCTGCGCGGACATGGGCGCTCCCGACCGGCTGCGCTGCGG	29.8*	DB 13;	Length 2175;	
230	GGAGTGAAGGCGCAATGCTGTGG-CATGGGCGCTCTCACCGGCTGACCTGCTGG	29.8*	DB 13;	Length 2175;	
327	CCACTGTGCTTCCAGCTCTGTGTGGCAGATGTATCCCGCAGGGGTTCCAGGGGCTG	29.8*	DB 13;	Length 2175;	
289	CCGCTGTGCTCTGAGAGCTGTGTGGTGAATATACCCCTCAGGGGTTATGGACGTG	29.8*	DB 13;	Length 2175;	
387	CCTCACCCCGGGGACCTGGAGAGAGAGAGAGTCCCTGTCCCGAGGAAATTAACAC	29.8*	DB 13;	Length 2175;	
349	CCTCACCTTGAAGGAGAGAGAGAGATGTGTGTGTCCCGAGGAAATTAATCAC	29.8*	DB 13;	Length 2175;	
447	CCGCAAAATAGACCAATTTGCTGCAACCAAGGCCCAAAAGTACTTCTGTCAATGAC	29.8*	DB 13;	Length 2175;	
409	CCTCAAAATTAATTCATTTGCTGTGACCAAGTGCACAAAGGAACTTCTGTCAATGAC	29.8*	DB 13;	Length 2175;	
507	TGTCCGGGCTCCAGGGGAGAGACAGGACTGCAAGGGTGTGTCCTCTGACCTTAC	29.8*	DB 13;	Length 2175;	
469	TGTCCAGGCGCCGGGAGAGATACGGAATGCGAGGAGGTGAGAGCGGCTCTTACCG	29.8*	DB 13;	Length 2175;	
567	TGGAGAACCAATCTCAGACGATGCTGAGCTGCTCCAGAGTCCCGGAGCGAAATGTT	29.8*	DB 13;	Length 2175;	
529	TCAAGAAACCACTTCAAGACCTGCTCAGCTGCTTCAAAATGCGAAAGGAAATGG	29.8*	DB 13;	Length 2175;	
627	GTGAGATTTGCGCTTGTGTGTGTGAGACCGGAGCACTGTGTGCGGCTGCAAGAA	29.8*	DB 13;	Length 2175;	
589	GTGAGATCTCTTTCTTTCAGAGTGGACCGGAGCAACGTTGTGTGTGTGTGTGT	29.8*	DB 13;	Length 2175;	
687	TACCGGAAATCTGAGGAGTGAATAAGCTTCCGAGTGTGAATCTGCAAGCTCTGT	29.8*	DB 13;	Length 2175;	
649	TACCGGAAATTTTGAAGTGAATACTTTTCCAGGCTTCAATTCAGGCTCTGTCT	29.8*	DB 13;	Length 2175;	
747	GGACAGTGAATATCTCTGCGAGAGAGAGAGACCAATCTGCACTGCTATATGGG	29.8*	DB 13;	Length 2175;	
709	GGGACCGTGAACCTCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	29.8*	DB 13;	Length 2175;	
807	TTCTTTCTTAAAGCGCGCAAGTCACTCTCTGTGATGATTTGAAGAA--CAAGAG	29.8*	DB 13;	Length 2175;	
769	TTCTTTCTTAAAG	29.8*	DB 13;	Length 2175;	



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Qy 864 GAGAGATTATGTCACACCGACCTTCACTGGTAAAGACTCTCAGAGACCGACCTACA 923
Db 869 ACGAAGTTGTGCTTACCCCAAGTTAGATGTTAAAGGCACTGAGGACTCAGGACCA 888
Qy 924 GTACTATTACCCCTGTGTATGTTCTTGGGCTTTGCTGGGATCTTGGCTGTGTC 983
Db 889 GTGCTGTGGCCCTGTGATTTCTTTGGTCTTTGCTTTTATCCCTCTTCACTTGT 948
Qy 984 TTAGATGTCGTACAGGGGTGAGGCGCAAGCTTACTCATTTGTTGGGGAGTGG 1043
Db 949 TTAATGTAATCGTACCAAGGAGGAGTCAAGCTTACTCATTTGTTGGGAAATCG 1008
Qy 1044 ACTGTGTAAAGAGGGGAGCGACAGAA-----CTCTGTGTCCCGGCCCAAGCTTC 1094
Db 1009 ACACGTGAAAAAGAGGGGAGGCTTGAAGAACTACTACTTAAAGCCCTGGCCCAAAACCA 1068
Qy 1095 AACCCACACCAACCATCTGCTTCACTGCTCAGCTCCCAAGTTCCAGTCTGTCTCCATTCCC 1154
Db 1069 AGCTTCACTGCCACTTCAAGAGCTTCAACCCCACTGGGCTTCAAGTCCCGTCCAGTTCC 1128
Qy 1155 CCTTCACTCTCTGTGACCGGTCCAACTTGGAG-----CGGTGGCATCTTCCCTCC 1205
Db 1129 ACTTTCACCTTCAAGTCCCACTTAAACCCCGGTGACTGTCCCACTTGTGGGCTCCGCG 1188
Qy 1206 AGCAGAGAGCGCCCGCCCATCTTAAAGCTGAGCCCATCTTCCCGGAGCTTCCGAGCTCC 1265
Db 1189 AGAGAGGTGGCAACCACTTATAGGGGGCTGACCCCATCTT----- 1229
Qy 1266 ACCCACTCTGTATCCCCGGGGGCTTCCGGCTTCCAGCCCACTCTGTATCCCCGGGGGCTTCCG 1325
Db 1230 -----TGCACACACCTTC 1242
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Db 1243 GCTTCAGACCCCATCTCCCAACCCCTTCAAGAGTGGAGAGACAGCGCCACA---AGCCA 1299
Qy 1386 GATCAGCTTCGCGGATGCGGACCCCGGACCTCTGTAACGCGGTGTGAGAGCGCTGCCCCG 1445
Db 1300 CAGAGCTTGAACATGATGATGACCCCGGAGCGTGTAGCGCTGTGTGAGAAAGTGTGCCCCG 1359
Qy 1446 TCGCGCTGGAAGAGTGTGTCGCGGCTGGAGCTGAGCGAGACAGAGATGAGAGCGCTG 1505
Db 1360 TTGCGCTGGAAGAAATTCGTGCGGCGCTTGAAGGCTGAGCGACACAGAGATTCATGCGCTG 1419
Qy 1506 GAGCTGGAAGAACGGCGGACCTGGCGGAGGCGGAGTACAGATGCTGGCGGCTGGGCG 1565
Db 1420 GAGCTGCAAGAACGGGCGCTGCTGGCGGAGCGCAATACAGATGCTGGCGACCTGGAGG 1479
Qy 1566 CGGCGCACGCGCGCGCGGAGGCGACGCTGAGCTGTGGCGCGGCTCTCAGGAGCATG 1625
Db 1480 CGGCGCACGCGCGCGCGGAGGCGACGCTGAGCTGTGGAGCGGTGCTCCGCAATG 1539
Qy 1626 GACCTGTGGGTTGCTGTAAGAAACATAGAGAGCGCTGGTGGCGCGCGCTTCCGCG 1685
Db 1540 GACCTGTGGGCTGCTGCTGAGAGACATCGAGAGGCGCTTGGCGCGCGCGCTTCCGCG 1599
Qy 1686 TCGGAGCGCGCGCTTCTCTGTGTAAGCGCGCGCGCTTCCGAGCTGGCGGCGCTTCCGCGCGCTG 1745
Db 1600 CCGCGCGCGCAATCTTCTCAGATGAGGCTGCGCGCGGCACTTAAAGACCGTCTG 1659
Qy 1746 C 1746
Db 1660 C 1660

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RESULT 7  
US-09-880-107-2360

; Sequence 2360, Application US/09880107  
; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darcí T.

; APPLICANT: Vockley, Joseph G.

; APPLICANT: Scherf, Uwe

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; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 2360
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M58286
US-09-880-107-2360

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Query Match 29.7%; Score 725.8; DB 10; Length 2111;  
Best Local Similarity 70.0%; Pred. No. 5.6e-174;  
Matches 1120; Conservative 0; Mismatches 387; Indels 92; Gaps 7;

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Qy 148 TGTCCCGCCCGACGTCTCAACCTTCCACTCCCGACCCGAGGCCGGGCTTCACTGGACA 207
Db 41 TCTCTATGCCGAGTCTCAACCTTCAACTGTCACTCCCAAGGCACTTGGAGCTCTGGAC 100
Qy 208 TACCGAGAGACCGTGTGTCTCACTGTCCGCGGCGCCCACTGCCC-CAGCCCTGATGGG 266
Db 101 AGACCGAGTCCCGGAGAGCCCGACGACTGCGCTGCCACACTGCTTGAAGCCCAATGGG 160
Qy 267 GGATTGAGAGGCGACAGTGGCCGAGATGGGCTTCCCAACCGTGGCTGCTGCTGCTG 326
Db 161 GGAATGAGAGGCGCTACTGTGTCTGG-CATGGGCTTCTTCCACCGTGTGCTGACTGCTG 219
Qy 327 CCACTGTGCTTCCAGCTCTGTGTGAGATGTGTACCCCGAGGGGTTTCAAGGCTGTGTC 386
Db 220 CCGCTGGTGTCTCTGAGACTGTGTGGAAATATACCCCTCAGGGGTTATTTGACTGGTC 279
Qy 387 CCTCACCCCGGGGACCTGAGAGAGAGAGAGTCCCTGTCGCCCAAGGAAATATATACAC 446
Db 280 CCTCACTTAAAGGAGCAGGAGAGAGAGATGATGTGTGTCCCAAGGAAATATATATCAC 339
Qy 447 CCGCAAAATAGCACCATTTGTGTGACCAAGTCCCAAAAGGTACTTACTTACATATGAC 506
Db 340 CTTCAAAATATTTGATTTGTGTATCCAGATGCTTCCAAAGGAACTTACTTATACATGAC 399
Qy 507 TGTTCGGGTTCAGAGCGGAGACAGGACTGACGGGTGTGTGCTTGGCACTTACATGCCC 566
Db 400 TGTCCAGGCGCGGAGGAGATACGAGACTGACAGGAGTGTGAGACGGGCTCTTACACGCT 459
Qy 567 TTGAGAAACCATCTCAACAGATGTCTGAGCTTCCAGTGTCCGAGTCCGAGAGAAATTTCCAG 626
Db 460 TCAGAAACCACTTCAAGCACTGTCTTCAAGTGTCCAAATGCTCCAAAGGAAATGGGTAG 519
Qy 627 GTGAGATTTTGCCTTGTGTGTGAGGACCGGAGCACTGTGTGCTGCGCTGAGAGAAACAG 686
Db 520 GTGAGATCTTCTTGTGACAGTGTGACCGGAGCACTGTGTGTGCTGCGCTGAGAGAAACAG 579
Qy 687 TACCGGGAATACGGGAGTGAATGCTTCCGATGTGTGAATCTGACGCTTGTCTCAAT 746
Db 580 TACCGGATTAATTTGAGAGTGAATCTTTCAGATGCTTCAATTCAGGCTTGTCTCAAT 639
Qy 747 GGCACAGTGAATATCCCTGCGAGAGAGAGAGACACATCTGCCACTGCAATATGGCC 806
Db 640 GGGACCGTGCACCTCTCTGCGAGAGAGAGAGAGACACATCTGCCACTGCAATATGGCC 699
Qy 807 TTTCTTTCTTAAAGGCGCAAGTGCATCTCTGTATGATTTTAAAGAA---CAAGGAGTGC 863
Db 700 TTTCTTTCTTAAAGGAGAGAGTGTGTCTCTGTATGTAATCTTAAAGAAAGCTGAGTGC 759
Qy 864 GAGAAATTATGTCCAAACCGGACCTTCAACTGTGTAAGACTCTCAGAGACCGAGCACTACA 923

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Db	541	TCCTGTACTACTGTAAAGAAAAGCTCGAGTGCACGAAAGTTGCTACCCGACATTGAG	600
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Db	891	ACTGTAAAGAAGCTCTCAGAGACCCAGGACACTACAGTACTTAAACCCCTGGTATTTGTCTTC	950
Qy			
Db	601	AATGTAAAGGGGACAGAGAGACTCAGAGCACACAGTGTGTGCCCCCTGGTCAATTTTCTTT	660
Qy			
Db	951	GGGCTTTGACCTGGCAATCCCTGGCTCTGTCGHTAGATGTCGCTACAGAGGGTGAAG	1011
Qy			
Db	1011	CCCAAGCTCTACTCCATCATATTGCGGGGAGTGCAGCTTGTTGTAAGAGGGGAGCCAGAA	1070
Qy			
Db	721	TCCAAGCTCTACTCCATTGTTGTGGGAAATGACACCTCGAAAAGAGGGGAGGCTTGA	780
Qy			
Db	1071	-----CTCTGTGTCCCGGCCCCCAGGCTTCAACCCACACCACTCTGCTTCAGC	1122
Qy			
Db	781	GGAACTACTACTAABCCCCCTGGCCCCCAACCCAGCTTCAAGTCCACCTCAGGCTTCAAC	840
Qy			
Db	1122	TCCACCCCAAGTTCAGTCTGTCTTCACANTCCCTTCATCTCTGTACAGGCTTCAC	1181
Qy			
Db	841	CCCACTCCGAGCTTCAAGTCTGTCTTCACANTCCCTTCATCTCTGTACAGGCTTCAC	900
Qy			
Db	1182	TTCCGAG-----CCGTGCATCTCCCTTCACAGAGACGGCCCCCATCTAAAG	1233
Qy			
Db	901	CCCCGTGACTGTCCCACTTTGGGGCTCCCCGACAGAGGTGGACACCTTATCAGGGG	960
Qy			
Db	1233	GCTGGCCCCCATCTCTCCCGGGGCTTCCGGCTTCACCCACCTCTGTACCCCGGGGCTCCG	1293
Qy			
Db	961	GCTGACCCCATCTCTTGCACAGACCTCTGGCTTCGACCCCATCCC-----	1004
Qy			
Db	1293	GCCTCCACCCACCTCTGTACCCCGGGGCTCCGGGCTCCAGCCACCTCTGCACCCCATGTT	1353
Qy			
Db	1005	-----CAACCCCTTT	1011
Qy			
Db	1353	CAGAAAGTGGAAAGCAGCGCCCCCAGCGCCCGATACAGCTCGGGATGTCGACCCCGCG	1411
Qy			
Db	1015	CAGAAAGTGGAGAGACAGCCGCCACA---AGCCACAGAGCTTACACTGATATACCCCGG	1077
Qy			
Db	1413	ACCCTGTACGCGGTGTGTGACGCGCTGCCCTCCGCTCGCGCTGAGAGAGATTTGTTGCCGCG	1477
Qy			
Db	1072	ACGCTGTACGCGGTGTGTGAGAAACGTGCCCGCTTGCCTGTGAAAGGAATTCGTGCCGCGC	1133
Qy			
Db	1473	CTGGGACTGAGAGGACACAGATTCGAGCGGCTGTGAGCTGTGAGAAACGGGGCCACTCTGCC	1533
Qy			
Db	1132	CTAAGGCTGAGAGGACACAGAGATTCATCGCTGTGAGCTGTGCAAAACGGGGCTGCTGCCG	1193
Qy			
Db	1533	GAGGGGACGTACAGCATGCTGTGCGGGCTGTGCGGCGGCGGACGCGCGCGCGAGGCGACG	1593
Qy			
Db	1192	GAGGGGCAATACAGATGTGTGCGACCTGTGAGAGCGGCGCACCCCGCGGCGCGAGGCGACG	1253
Qy			
Db	1593	CTGAGCTGTCTGGGCGCGCTGTCTCAGAGGACATGTGCTGGATTGCTCTGAAAAACATA	1653
Qy			
Db	1252	CTGAGAGCTGTCTGGGACCGGTGTCTCGCGGACATGTGAGACTGTCTGGGCTGCTGTGAGGACATC	1311
Qy			
Db	1653	GAGGAGGCGCTGTGGGTGTGCGCGCGCGCGCTCTGCTCGAGAGCCCGGCTTCTGTGTGA	1709
Qy			
Db	1312	GAGGAGGCGCTTTGGCGGCGCGCGCGCTCTCGCGCGCGCGCCACGATCTTCTCAGATGA	1368
Qy			

RESULT 10

US-09-429A-1

; Sequence 1, Application US/09899429A

; Patent No. US20020169118A1

; GENERAL INFORMATION:

; APPLICANT: Hauptmann, Rudolph

; APPLICANT: Himmler, Adolph

; APPLICANT: Maurer-Fogy, Ingrid

; APPLICANT: Strizowa, Christian

; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for

; TITLE OF INVENTION: Them

; FILE REFERENCE: 98-385-J

; CURRENT APPLICATION NUMBER: US/09/899,429A

; CURRENT FILING DATE: 2001-07-03

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1 PRIOR APPLICATION NUMBER: 09/792,356
2 PRIOR FILING DATE: 2000-02-23
3 PRIOR APPLICATION NUMBER: 08/477,639
4 PRIOR FILING DATE: 1955-06-07
5 PRIOR APPLICATION NUMBER: 08/383,676
6 PRIOR FILING DATE: 1995-02-01
7 PRIOR APPLICATION NUMBER: 08/153,287
8 PRIOR FILING DATE: 1993-11-17
9 PRIOR APPLICATION NUMBER: 07/821,750
10 PRIOR FILING DATE: 1992-01-02
11 PRIOR APPLICATION NUMBER: 07/511,430
12 PRIOR FILING DATE: 1990-04-20
13 NUMBER OF SEQ ID NOS: 97
14 SOFTWARE: PatentIn Ver. 2.0
15 SEQ ID NO 1
16 LENGTH: 1368
17 TYPE: DNA
18 ORGANISM: Homo sapiens
19 FEATURE:
20 NAME/KEY: CDS
21 LOCATION: (1)..(1365)
22 NAME/KEY: sig_peptide
23 LOCATION: (1)..(87)
24 NAME/KEY: misc_feature
25 LOCATION: (88)..(120)
26 OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
27 OTHER INFORMATION: extracellular proteases following secretion
28 NAME/KEY: misc_feature
29 LOCATION: (606)..(633)
30 OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
31 OTHER INFORMATION: extracellular proteases following secretion
32
33 US-09-899-429A-1

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Query Match	28.1%;	Score 685.4;	DB 10;	Length 1368;
Best Local Similarity	71.1%;	Pred. No. 8.9e-164;		
Matches 1021;	Conservative 0;	Mismatches 326;	Indels 90;	Gaps 5

QY	29	ATGGAGCTCCCAACCGTGTCTGGACCTGTGTCTGGACACTGGAGCTTTCAGAGCTTTGGCA	353
Db	1	ATGGAGCTCTCAACCGTGTCTGGACCTGTGTCTGGACACTGGAGCTTTCAGAGCTTTGGTG	60
QY	354	GATGTGTACCCCGCAGGGGTTCAAGGGCTGTGTCCTCAACCCCGGGGACCTGGAGAAAGA	413
Db	61	GGAAATTACCCCTCAGGGGTTATTGGACTGTGTCCTCACTAGGGGACAGGGAGAAAGA	120
QY	414	GAGAGTCCGTGTCCCAAGAAATAATACACCCGCAAAATTAGACATTTGTGTGACC	473
Db	121	GATAGTGTGTGTCCCAAGAAATAATACACCTCAAAATTAATGCAATTTGTCTTGACC	180
QY	474	AAGTGCACAAAGTAACCTATCTGTCAATGACTGTCCGGGTCCAGGGCGAGACACGGAC	533
Db	181	AAGTGCACAAAGTAACCTATTGTACATGACTGTCCAGGCCCGGGGCGAGTAACGGAC	240
QY	534	TGAGAGGTGTGTGCCCCCTGGCACCTACACCTTCCTTGGAGAAACATCTCACAACATGTCTG	593
Db	241	TGAGAGGAATGTGAGAGCGGCTCTTCAACGGCTTCAGAAAACACCTCACAACCTGCTTC	300
QY	594	AGTGTCTCCAGGTGCGCGGACGAAATGTTTCCAGGTGAGATTTTCGCTTGTAATGTGAC	653
Db	301	AGTGTCTCCAAATGCGGAAAGAAATGGGTCAAGGTGGAGATCTCTTCTGCACAGTGGAC	360
QY	654	CGGGAACATGTGTGTGGGCTGTGAGAAAGAACAGATACCGGGAAATCTGGGGTGGAACTGGC	713
Db	361	CGGGAACACGTGTGTGTCGTGACAGAAAGAACAGTACCGGCAATTAATGTGAGTGAAGAACTTT	420
QY	714	TTCCGGTGTCTGAACGTGACGCTCTGTCTCCAAATGGCACAAGTGAATATCCCTGCAAGAG	773
Db	421	TTTCAATGTCTCAATTTGACGCTCTGTCTCCAAATGGGACCGTGACCTCTCTGCAAGAG	480
QY	774	AGACAGGAACAATCTGCGCACTGCGCATATGGGCTTTCTTTCTTAAAGGCGCAAGTGATC	833
Db	481	AAACAGGAACAACGTGTGACCTGTCCATCAGATTTCTTTCTTAAAGAAACGAGTGTGTC	540



834 TCCTGTCTGATGTTGAAGA---CAAGAGTCCGGAAGTATATGTCACACCCGACCTTCA 890  
541 TCCTGTCTGATGTTGAAGAAGCTTGAGATGACGAAAGTGTGCTTACCCGAGATTAG 600  
891 ACTGTAAGACTCTCAGAGCCAGGACCTACAGTACTATTACCCCTGATGTTGCTTC 950  
601 AATGTTAAGGACATGAGAGCTCAGGACACAGAGTGTGCTTCCCTGATGTTTCTT 660  
951 GGGCTTGTGCTGAGATCTTGTGCTCTGTGCTCTTGAAGATGTGCTTACAGCGTGAAG 1010  
661 GGTCTTGTGCTTATCT 720  
1011 CCAGAGCTTACT 1070  
721 TCAGAGCTTACT 780  
1071 -----CTCTGTGCT 1121  
781 GGAAGTCTACTAGAGCCCT 840  
1122 TCAGAGCTTACT 1181  
841 CCAGAGCTTACT 900  
1182 TTGGAG-----CCGTGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1232  
901 CCAGAGCTTACT 960  
1233 GCTGAGCTTACT 1292  
961 GCTGAGCTTACT 1004  
1293 GCTGAGCTTACT 1352  
1005 -----CAAGAGCTTACTAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1014  
1353 CAGAGAGTGAAG 1412  
1015 CAGAGAGTGAAG 1071  
1413 ACCGTGATGAG 1472  
1072 ACCGTGATGAG 1131  
1473 CTGAGAGTGAAG 1532  
1132 CTGAGAGTGAAG 1191  
1533 GAGAGAGTGAAG 1592  
1192 GAGAGAGTGAAG 1251  
1593 CTGAGAGTGAAG 1652  
1252 CTGAGAGTGAAG 1311  
1653 GAGAGAGTGAAG 1709  
1312 GAGAGAGTGAAG 1368

RESULT 12  
US-10-252-408-3  
; Sequence 3, Application US/10252408  
; Publication No. US20030082736A1  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, Craig A.  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS  
; FILE REFERENCE: A-71592  
; CURRENT APPLICATION NUMBER: US/10/252,408  
; PRIORITY FILING DATE: 2002-09-24  
; PRIORITY FILING NUMBER: US/08/406,824  
; PRIORITY FILING DATE: 1995-03-20

PRIOR APPLICATION NUMBER: US 08/255,849  
; PRIOR FILING DATE: 1994-06-08  
; PRIOR APPLICATION NUMBER: US 07/860,710  
; PRIOR FILING DATE: 1992-03-30  
; PRIOR APPLICATION NUMBER: US 07/523,635  
; PRIOR FILING DATE: 1990-05-10  
; PRIOR APPLICATION NUMBER: US 07/421,417  
; PRIOR FILING DATE: 1989-10-13  
; PRIOR APPLICATION NUMBER: US 07/405,370  
; PRIOR FILING DATE: 1989-09-11  
; PRIOR APPLICATION NUMBER: US 07/403,241  
; PRIOR FILING DATE: 1989-09-05  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 3  
LENGTH: 1368  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1365)  
; OTHER INFORMATION:  
; NAME/KEY: mac\_peptide  
; LOCATION: (121)..()  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (1)..(120)  
; OTHER INFORMATION:  
US-10-252-408-3

Query Match 28.04; Score 683.8; DB 14; Length 1368;  
Best Local Similarity 71.04; Pred. No 2.3e-163;  
Matches 1020; Conservative 0; Mismatches 327; Indels 90; Gaps 5;  
294 ATGGGCTCTCCCAACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 353  
1 ATGGGCTCTCCCAACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60  
354 GATGTGATACCCCGAGAGGCTTACAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 413  
61 GGAATATACCCCGAGAGGCTTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
414 GAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473  
121 GATGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
474 AAGTGCACAAAGATCTATCTGTACATGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533  
181 AAGTGCACAAAGATCTATCTGTACATGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
534 TGAAGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593  
241 TGAAGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
594 AGCTGTCTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653  
301 AGCTGTCTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
654 CGGAGACATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713  
361 CGGAGACATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
714 TTCGGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 773  
421 TTCGGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
774 AGACAGAGACATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 833  
481 AAGCAGACATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
834 TCCTGTCTGATGTTGAAGA---CAAGAGTCCGGAAGTATATGTCACACCCGACCTTCA 890



QY 1182 TTGGAG-----CCGTGCATCTCTCCAGCGAGCGCCCGCCCATCTAAAG 1232  
DB 901 CCGGTACTGTCCCACTTGGCGCTCCCGCAGAGAGTGGACCACTTATCAGGGG 960  
QY 1233 GCTGGCCCACTCTCCGGGGGCTCCGGGCTCCCACTCTTACCCGGGGCTCCG 1292  
DB 961 GCTGACCCCACTCTTGGGAGACGCGCTCGCTCCGACCCCATCTCC----- 1004  
QY 1293 GCCTCCACCACTCTGTACCCCGGGGCTTCGCGCTCCACCACTCTGACCCCACTT 1352  
DB 1005 -----CAACCCCTT 1014  
QY 1353 CAGAACTGGGAAGCGACGCGCCCGACGCGCCGATCACTCGGATGCCGACCCCGG 1412  
DB 1015 CAGAACTGGGAGGACAGCGGCCCA---AGCCACAGAGCTTACATGATGACCCGCG 1071  
QY 1413 ACCCTGACGCGGTGGAGGAGCGGCGTCCCGCTCGGCTGGAAGAGTTGGTGGCGG 1472  
DB 1072 ACCTGTACGCGCTGGTGGAGAGAGTGCCTCCGCTTGGCGTGAAGGAAATTCGTGGGCGC 1131  
QY 1473 CTGGACTGAGCGAGCAGAGATGAGCGGCTGGAGCTGGAGAAAGGGCGCACTGCGC 1532  
DB 1132 CTAGGGCTGAGCGAGCAGAGATGATCGCTGAGAGCTGAGAAAGGGCGCTGCTGCGC 1191  
QY 1533 GAGCGCAGTACAGCATCTGCGCGCTTGGCGGCGGCGGCGCGCGCGGAGGCGAG 1592  
DB 1192 GAGCGCGAATACAGCATCTGCGCGAGCTGGAGGCGGCGGCGCGCGCGGAGGCGAG 1251  
QY 1593 CTGGAGCTGCGGGCGGCGGTCTCAGGGAGATGAGCTGCTGGTAAAGTAAAGTAA 1652  
DB 1252 CTGGAGCTGCGGGAGCGGCTCTCGAGACGTGAGCTGCGGCTCTGAGAGATC 1311  
QY 1653 GAGAGCGCTGAGTGGCGCGCGCTCGCTGCGGCGCGCTCTCTCTGAGTGA 1709  
DB 1312 GAGAGCGCTGTTGGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCATGTA 1368

RESULT 14  
US-10-157-305A-18  
; Sequence 18, Application US/10157305A  
; Publication No. US20030166099A1  
; GENERAL INFORMATION:  
; APPLICANT: Sabbadini, Roger A.  
; APPLICANT: Surber, Mark W.  
; APPLICANT: Neil Berkley  
; APPLICANT: Anca M. Segall  
; APPLICANT: Robert Klepper  
; TITLE OF INVENTION: MINICELL COMPRISING MEMBRANE PROTEINS  
; FILE REFERENCE: MPX. 008DV1  
; CURRENT APPLICATION NUMBER: US/10/157,305A  
; PRIOR FILING DATE: 2002-05-28  
; PRIOR APPLICATION NUMBER: 60/293,566  
; PRIOR FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: 60/359,843  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 10/154,951  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 258  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 1380  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-157-305A-18

Query Match 25.7%; Score 628; DB 12; Length 1380;  
Best Local Similarity 70.5%; Pred. No. 3.1e-149;  
Matches 954; Conservative 0; Mismatches 310; Indels 90; Gaps 5;

QY 377 GGGGCTGTCTCCCTCACTCCCGGAGCTGGAGAGAGAGAGTCCCTGTCCTCCCAAGAAA 436  
DB 53 GGAGCTGTCTCTCACTTGAAGGAGCAGGAGAGAGAGATGTGTGTCTCCCAAGAAA 112

QY 437 ATATTAACACCCGCAAAATAGACCAATTGCTGACCAACGAGGCGACAAAGTACTATCT 496  
DB 113 ATATATCAACCCCTCAAAATATATGATTTGCTGTACCAATGGCGACAAAGAACTACTT 172  
QY 497 GTACATGATCTGTCCGGGTCCAGGGCGAGACAGGACTGACAGAGTGTGTCTCCCTGGAC 556  
DB 173 GTACAAATGATCTGTCCAGGCGCGGGGAGATGAGATGACAGGAGAGTGTGAGAGCGCTC 232  
QY 557 CTACACTGCTTGGAGAAACATCTCAGACGATGCTGAGCTGCTCCAGGTGGCGGAGCA 616  
DB 233 CTTCACGCTTCCAGAAACCACTTCAGACCTGCTCTGAGCTGCTCCAAATGCGAAAGGA 292  
QY 617 AATGTTCCAGTGGAGATTTGCGCTGTGTAGTGAACCGGAGACATGTGTGCGCTGACG 676  
DB 293 AATGGGTCAGTGTGAGATCTCTTCTTGACAGTGAACCGGAGACACGCTGTGTGCTGACG 352  
QY 677 GAAGAACATGATCCGGGAAATACGTGGGTGAATCTGCTTCGGTGTGAATGACGCT 736  
DB 353 GAAGAACATGATCCGGGATTAATGAGTGAACCTTTTCAGTGTCTCAATTGACGCT 412  
QY 737 CTGTCCCAATGGGACAGTGAATATCCCTGCGCAGGAGAGACAGGACCACTGCGCAC 796  
DB 413 CTGCTTAATGGAACGCTGACCTCTCTGCGCAGGAGAAACAGAACCGGTGTGACCTG 472  
QY 797 CCATATGGGCTTCTTTCTTAAAGGCGCAAGTCACTCTCTGTCAATGATTTGAAGAA--- 853  
DB 473 CCATGCAAGTCTTTCTTAAAGAAACAGTGTGTCTCTGTAGTAACTGAAGAAAG 532  
QY 854 CAAGAGTGGAGAGATTAATGTCMAACCGGACCTTCAACTGTGAAGACTCTCAGAGACC 913  
DB 533 CTTGGAGTGCACAGAGTGTGCTTACCCGATTTGAGAAATGTTAAGGCGACTGAGGACTC 592  
QY 914 AGGCACTACAGTACTAATTAACCTGGTGAATGTCTTGGGCTTGGCTGCGCATCTTGGC 973  
DB 593 AGGCACTACAGTCTGTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 652  
QY 974 CTCTGTCTTGTAGCATGTGCTACAGCGGTGGAAGCCCAAGCTCACTCAATTTG 1033  
DB 653 CTTCAATGTTAATGATGATGCTACCAAGGTTGGAAGTCCAACTCACTCAATTTGTTG 712  
QY 1034 CGGCACTGCACTCTGTGAAGAGGGGAGCCAGAACTCT-----GCTCCGCGC 1084  
DB 713 TGGGAATTCACACCTGAAGAAAGAGGGGAGCTTGAAGAACTACTAAGCCCTCGGC 772  
QY 1085 CCAGAGCTTCAACCCACCAACCAACCATCTGCTTACGCTTCAACCCCAAGTTCAGTCTCT 1144  
DB 773 CCAGAACCAAGCTTCAAGTCCACTCCAGGCTTACCCCACTTGGGCTTCAAGTCCGT 832  
QY 1145 CTCCATTTCCCTTACATCTCTGTGACCGGTCAACTTGGAGCGG-----TCGC 1195  
DB 833 GCCCATGTTCACTTCACTCCAGCTCCAGCTCACTTATACCCCGGTGATGTGCCAATTTGC 892  
QY 1196 ATCTCTCTCCAGGAGAGCGGCGCGCCCATCTTAAAGCTGTGCGCCCATCTCCCGGGCC 1255  
DB 893 GGTCTCCCGCAGAGAGGTGGCAACACCTTATCAGGGGGCTGACCCCATCTTCGACAGC 952  
QY 1256 TCGGAGCTCCAGCACTCTGTACCCCGGGGCTTCGGGCTTCAACCACTCTGTACCC 1315  
DB 953 CTGCGCTCTCGACCCCATCTCC----- 973  
QY 1316 GGGGCTTCGGCTCCACCACTCTGCAACCCAGTTTCAGAAATGGGAAGCCAGCGCCC 1375  
DB 974 -----CAACCCCTTCAAGAAATGGGAAGACAGCGCCCA 1006  
QY 1376 CAGCGCCCGGATACGTGCGGATGCGGACCCCGGACCTGTACCGGTGTGAGACGG 1435  
DB 1007 CA---AGCCACAGAGCTGAGACACTGATGACCCCGGACGCTGTACGCGGTGTGAGAA 1063  
QY 1436 CGTGGCCCGGTGCGGTGGAAGAGTGTGTGCGGCGCTGTGAGCTGACGAGACAGAT 1495  
DB 1064 CGTGGCCCGGTGTGCGGTGGAAGAAATTCGTGCGGCGCTTGAAGGCTGAGCGACAGAT 1123



QY 1496 CGAGCGCTGAGCTGAGAAAGGCGCCACCTGCGCGAGCGCAGTACACATGCTGCG 1555  
 DB 1124 CGATCGCTGAGCTGCGAAACGCGCGCTGCTGCGCGAGCGCAATACATGCTGCG 1183  
 QY 1556 GGCCTGCG 1615  
 DB 1184 GACCTGCG 1243  
 QY 1616 CAGGAGCATGAGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1675  
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 DB 1304 CGCCTCG 1337

RESULT 15  
 US-10-157-391-18  
 : Sequence 18, Application US/10157391  
 : Publication No. US20030166279A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Sabbadini, Roger A.  
 : APPLICANT: Neil Berkley  
 : TITLE OF INVENTION: MINICELL-BASED TRANSFECTION  
 : FILE REFERENCE: MPX. 008DV14  
 : CURRENT APPLICATION NUMBER: US/10/157,391  
 : CURRENT FILING DATE: 2002-05-28  
 : PRIOR APPLICATION NUMBER: 60/293,566  
 : PRIOR FILING DATE: 2001-05-24  
 : PRIOR APPLICATION NUMBER: 60/359,843  
 : PRIOR FILING DATE: 2002-02-25  
 : PRIOR APPLICATION NUMBER: 10/154,951  
 : PRIOR FILING DATE: 2002-05-24  
 : NUMBER OF SEQ ID NOS: 257  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 18  
 : LENGTH: 1380  
 : TYPE: DNA  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Fusion protein  
 US-10-157-391-18

Query March 25.7% Score 628; DB 12; Length 1380;

Best Local Similarity 70.5%; Pred. No. 3.1e-149; Matches 954; Conservative 0; Mismatches 310; Indels 90; Gaps 5;

QY 377 GGGGCTGCTCCTCACCAGGCGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 436  
 DB 53 GGAAGTGGTCTCCTCACCAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 112  
 QY 437 ATATTAACACCCGCAAAATAGACCATTTGCTGCAACCAAGTGCACCAAGTACTATCT 496  
 DB 113 ATATTAACACCCGCAAAATAGATTTGCTGCAACCAAGTGCACCAAGTACTATCT 172  
 QY 497 GTACAAATGCTGCTGCGGCTGCAAGGCGGAGAGACAGGAGTGCAGGCGGCTGCGGAC 556  
 DB 173 GTACAAATGCTGCTGCGGCTGCAAGGCGGAGAGATGCGAGGAGTGCAGGCGGCTG 232  
 QY 557 CTACACTGCTGCTGAGAAACATCTCAGACGATGCTGAGCTGCTCAGAGTCCCGGAGCA 616  
 DB 233 CTACACTGCTGCTGAGAAACATCTCAGACGATGCTGAGCTGCTCAGAGTCCCGGAGCA 292  
 QY 617 AATGTTCCAGTGAAGATTTGCGCTTGTGTAGTGAACCGGAGCACTGTGTGCGGCTGAG 676  
 DB 293 AATGTTCCAGTGAAGATTTGCGCTTGTGTAGTGAACCGGAGCACTGTGTGCGGCTGAG 352  
 QY 677 GAAGAAACAGTACCGGAGAAATCTGGGAGTGAACCTGCTTCCGAGTCTGAAGTGAAGCT 736  
 DB 353 GAAGAAACAGTACCGGAGAAATCTGGGAGTGAACCTTTCAGAGTCTGAAGTGAAGCT 412  
 QY 737 CTGTCCCAATGAGCAGTGAATATCCCTGCGAGAGAGAGAGACAGACCATCTGCACTG 796

DB 413 CTGCTCAATGAGACCGTGACCTCTCTGCGAGAGAAACAGAAACACCGTGACACTG 472  
 QY 797 CCAATAGGCTCTTTCTTAAAGGCGCGAGTGAATCTCTGATATATTTAGAA--- 853  
 DB 473 CCAATAGGCTCTTTCTTAAAGGCGCGAGTGAATCTCTGATATATTTAGAAAG 532  
 QY 854 CAAGAGTGCAGAAAGTTATGTCACCCGACTTCAACTGTGTAAAGACTCTAGAGACC 913  
 DB 533 CTGAGTGCAGAAAGTTATGTCACCCGACTTCAACTGTGTAAAGACTCTAGAGACT 592  
 QY 914 AGGCACTACAGTACTATTAATCCCTGATGTTGCTTCTGCGGCTTTGCTGAGCATCTTGC 973  
 DB 593 AGGCACTACAGTACTATTAATCCCTGATGTTGCTTCTGCGGCTTTGCTGAGCATCTTGC 652  
 QY 974 CTGCTGCTCTTACAGTGTGCTTCAAGCGGTGAACCCGAGTCTTACATCATATTG 1033  
 DB 653 CTGCTGCTCTTACAGTGTGCTTCAAGCGGTGAACCCGAGTCTTACATCATATTG 712  
 QY 1034 CCGGCACTGCACTGTGTAAGAGAGGAGCGCAGAACTCT-----GATCCGCGC 1084  
 DB 713 TGGGAAATTCAGACCTGAAAGAGGAGGAGCTTGAAGAACTACTAGTAAAGCTTGC 772  
 QY 1085 CCGAGGCTTCAACCCGACCAACCAATCTGCTTCAAGCTTCAACCCGAGTCTTGC 1144  
 DB 773 CCGAAACCCGAGCTTCAAGTCTTCAAGGCTTCAACCCGAGTCTTCAAGTCTTGC 832  
 QY 1145 CTGCTATCCCTTCAATCTCTGATGACCGGTCAACTTGTGAGACCG-----TCGC 1195  
 DB 833 GCGCAATTCACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 892  
 QY 1196 ATCTCCCTTCAAGCAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1255  
 DB 893 GGTCTCCCGCAGAGAGAGTGCACCACTTATCAGAGGAGTGCACCACTTCTTGAAGACG 952  
 QY 1256 TCGGAGCTTCAACCACTTGTACCCCGGAGCTTCCGAGCTTCAACCACTTGTACCC 1315  
 DB 953 CCGGAGCTTCAACCACTTGTACCCCGGAGCTTCCGAGCTTCAACCACTTGTACCC 973  
 QY 1316 GGGGCTCTCGGCTTCAACCACTTGTACCCCGGAGCTTCAACCACTTGTACCCCGG 1375  
 DB 974 -----CAACCTCTTCAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1006  
 QY 1376 CAGGCGCGCGATCAGCTCGCGAGTGCAGACCCGCGACCTGTACCGGAGTGTGAGAG 1435  
 DB 1007 CA---AGCCACAGAGCTTATGACACTGATGACCCCGCAGCCTGTATCCCGTGTGAGAA 1063  
 QY 1436 GGTGCTCTCTGCGGTGAGAGAGTGTGTCGCGGCTGAGACTGAGCGACAGAGAT 1495  
 DB 1064 GGTGCTCTCTGCGGTGAGAGAGTGTGTCGCGGCTGAGAGCTGAGCGACAGAGAT 1123  
 QY 1496 CGAGCGCTGAGAGCTGAGAGAAAGGCGCGCACTTGCAGAGCGGAGAGAGAGAGAGAG 1555  
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 QY 1556 GGCCTGAGCGGCGAGCG 1615  
 DB 1184 GACCTGAGAGGCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1243  
 QY 1616 CAGGAGCATGAGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1675  
 DB 1244 CCGGAGCATGAGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1303  
 QY 1676 CCGCTGCGCGCTGCG 1709  
 DB 1304 CGCCTCG 1337

Search completed: September 15, 2003, 09:29:04  
 Job time : 454 secs







Dp	421	GGGCGTCCCCCGCTGAGACGGCGCTTCTTCTCTGAGCCAGGACCCGGAAGACT	480
Qy	1790	GGGAGATGCCCTTGTGACCTCTGTTTGTGTTTGTGTTTGTGAGAGGAGTCTTGA	1849
Dp	481	GGGAGATGCCCTTGTGACCTCTCTGTTTGTGTTTGTGTTTGTGAGAGGAGTCTTGA	540
Qy	1850	GGAGAGGACGATCTGTGGACGCACTGACCTGGTGTACTACACAGTATCATAGCTTT	1909
Dp	541	GGAGAGGACGATCTGTGGACGCACTGACCTGGTGTACTACACAGTATCATAGCTTT	600
Qy	1910	TCTCAGCTGCTGAGTGTGTCTGTGTGT	1939
Dp	601	TCTCAGCTGCTGAGTGTGTGTGTGTGT	630
RESULT 3			
LOCUS	CB439280	632 bp	mRNA linear EST 25-MAR-2003
DEFINITION	688899 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.		
ACCESSION	CB439280		
VERSION	CB439280.1	GI:29224127	
KEYWORDS	EST.		
SOURCE	Bos taurus (cow)		
ORGANISM	Bos taurus		
REFERENCE	Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.		
AUTHORS	1 (bases 1 to 632) Smith,T.P.L., Roberts,A.J., Echeerikamp,S.E., Chitko-Mckown,C.G., Wray,J.E. and Keale,J.W.		
TITLE	A second set of bovine ESTs from pooled-tissue normalized libraries		
JOURNAL	Unpublished		
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smithth@mail.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329. Plate: PQY8044 row: N column: 10 Seq primer: TAGAAGCAGACGTGAGG. Location/Qualifiers 1..632 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /issue_type="pooled" /lab_host="DH10B" /clone_id="MARC 6BOV" /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."		
FEATURES			
source			
Query Match	25.7%	Score 627.4;	DB 14; Length 632;
Best Local Similarity	99.8%;	Pred. No. 1.3e-97;	
Matches 628;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
Qy	1766	GTGCAGGACACCCGGGAAGATCTGCGAGATCCCTGTGAGACCTCGTTTGTGTTTGT	1825
Dp	632	GTGCAGGACACCCGGGAAGATCTGCGAGATCCCTGTGAGACCTCGTTTGTGTTTGT	573
Qy	1826	TTTTTCTGAGAGGAAGTCTTGAGAGGACGACGATCTGGCAGCACTGACCTGGTGC	1885
Dp	572	TTTTTCTGAGAGGAAGTCTTGAGAGGACGACGATCTGGCAGCACTGACCTGGTGC	513
Qy	1886	TACTCAGTCAGTATCATAGCTTTTCTCAGCTGCCCTGAGTGTGTGTGTGTAGTGTG	1945

Db	512	TACTACACTCAGGTGATACAGTCTTTCTCAGCTGCGTGAAGTGTGCTGTGTGTGAAGTGTG	455
Qy	1346	TGTCGTGCGTGCAGTGCAGTGTGTGTGTGTGTCTCTGTATATGTGGCTCTGTGTGATGTGAGATGT	2005
Db	452	TGTCGTGCGTGCAGTGCAGTGTGTGTGTGTCTCTGTATATGTGGCTCTGTGTGATGTGAGATGT	393
Qy	2006	GTGTACTCGTAGAGAGAGAGGCGAGTGTCCCGAGACCCAGAGGCAAGTGTGTGCGAAGATGTAG	2065
Db	392	GTGTACTCGTAGAGAGAGAGGCGAGTGTCCCGAGACCCAGAGGCAAGTGTGTGCGAAGATGTAG	333
Qy	2066	GGGCGCCCTGCTCTATTTGCTGTTTTTTTGGGCTTTGGAACTCAGCAAGCGCACTTGTGGG	2125
Db	332	GGGCGCCCTGCTCTATTTGCTGTTTTTTTGGGCTTTGGAACTCAGCAAGCGCACTTGTGGG	273
Qy	2126	AACCTTAGCTGTGTGCTCCCTGAGCCGGTTTTCGAGTAGATTAAGCATCTTTGTATTCACACTCTG	2185
Db	272	AACCTTAGCTGTGTGCTCCCTGAGCCGGTTTTCGAGTAGATTAAGCATCTTTGTATTCACACTCTG	213
Qy	2186	CACATTCACATCATTCGATCTGTGTATACATTAATTAAGAACTTTGTGGCCCTGTGACACCACT	2245
Db	212	CACATTCACATCATTCGATCTGTGTATACATTAATTAAGAACTTTGTGGCCCTGTGACACCACT	153
Qy	2246	GAACCTGTCCCGAGGAGGCGGAGAGCAGAGAAAAATGTGGGCTCTCCAGAGGAGCTAGCTG	2305
Db	152	GAACCTGTCCCGAGGAGGCGGAGAGCAGAGAAAAATGTGGGCTCTCCAGAGGAGCTAGCTG	93
Qy	2306	TTTCAGTTTCAGTTTCAGTGTGCTCAGTGTGTGTGCGACTCTTTTGGAGCCCTGTGAATGCAAGG	2365
Db	92	TTTCAGTTTCAGTTTCAGTGTGCTCAGTGTGTGTGCGACTCTTTTGGAGCCCTGTGAATGCAAGG	33
Qy	2366	ACTTCTGTAAATACACTTAATAATCTTCCAA	2394
Db	32	ACTTCTGTAAATACACTTAATAATCTTCCCA	4
RESULT 4			
CB169950/c			
LOCUS	CB169950	659 bp	mRNA linear EST 30-JAN-2003
DEFINITION	C216030001005.R1 CSEBQFN21 testes Bos taurus		linear mRNA sequence.
ACCESSION	CB169950		
VERSION	CB169950.1	GI:28156078	
KEYWORDS	EST.		
SOURCE	Bos taurus (cow)		
ORGANISM	Bos taurus		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Ruminantia; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.		
AUTHORS	1 (bases 1 to 659)		
TITLE	Adelson, D.L. and Gyll, C.A.		
JOURNAL	Bovine ESTs (Adelson and Gyll)		
COMMENT	Unpublished Contact: David L. Adelson Animal Breeding and Genetics Texas A&M University Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA Tel: 9799452616 Fax: 9798456970 Email: david.adelson@tamu.edu. Location/Qualifiers 1. 659 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon.9913" /clone_id="CSEBQFN21 /cvsu_id="CSEBQFN21 /note="Organ: testes; Vector: pBluescript SK+; Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert (5'-NNN...NNNinsert) GCCAATTGAGCTCCACCGCGGTGGCGGCGCGGCTGAG. Sequence 3' of the insert (AAGATTGATATACATTAATGATATACCTGACCTCGAG. normalized Rd 2 library, sequenced 3' with M13R primer."		
FEATURES			
SOURCE			
BASE COUNT	179 a	192 c	159 g
			129 t

## ORIGIN

Query Match 25.5%; Score 622.8; DB 14; Length 659;

Best Local Similarity 98.5%; Pred. No. 7,7e-97;

Matches 640; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

1769 CCAGGACACCCGGAAGATCTGCGAGATGACCCCTGAGACCTCTGTTGTTGTTT 1828  
 659 CCAGGACACCCGGAAGATCTGCGAGATGACCCCTGAGACCTCTGTTGTTT 600  
 1829 TTCT--GGAAGAGAGTCTTGGAGACGAGCATCTGGACCACTGACTGTC 1885  
 599 GTTCTGAGTGAAGAGTCTTGGAGACGAGCATCTGGACCACTGACTGTC 540  
 1886 TACTACTCAGTGTACATAGCTTTCTCAGCTGCTGATGATGATGATGATG 1945  
 539 TACTACTCAGTGTACATAGCTTTCTCAGCTGCTGATGATGATGATGATG 480  
 1946 TGTCTGCGTGCAGTGCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2005  
 479 TGTCTGCGTGCAGTGCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 420  
 2006 GTTACTCTGTGAGAGAGGCGGAGTGTGCGGAGCCCAAGCAGTGTTCGAGATG 2065  
 419 GTGTACTGTGAGAGAGGCGGAGTGTGCGGAGCCCAAGCAGTGTTCGAGATG 360  
 2066 GGGGCGCCCTGCTTATGCTGTTTGGGCTTGGAGAACTCAGCAGAGCGACTTGG 2125  
 359 GGGGCGCCCTGCTTATGCTGTTTGGGCTTGGAGAACTCAGCAGAGCGACTTGG 300  
 2126 AACCTAGCTGCGTCCCTGAGCCGTTTGGCAGTATAGCATCTTTGATCACTGT 2185  
 299 AACCTAGCTGCGTCCCTGAGCCGTTTGGCAGTATAGCATCTTTGATCACTGT 240  
 2186 CACATCTCATCTCACTCTGTATCACTAATAGAACTTTGTTGCTGCTGAGCACT 2245  
 239 CACATCTCATCTCACTCTGTATCACTAATAGAACTTTGTTGCTGCTGAGCACT 180  
 2246 GAACGTGCTCCGAGGAGCGGGGAGCAGAAATTTGGGCTTCCAGAGGAGCTAGCTG 2305  
 179 GAACGTGCTCCGAGGAGCGGGGAGCAGAAATTTGGGCTTCCAGAGGAGCTAGCTG 120  
 2306 TTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 2365  
 119 TTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 60  
 2366 ACTCTGTAAATATACATAAATCTTCAATTAAGCTTGCCTTGGAGGG 2415  
 59 ACTCTGTAAATATACATAAATCTTCAATTAAGCTTGCCTTGGAGGG 10

## RESULT 5

CB455341

LOCUS 631 bp mRNA linear EST 26-MAR-2003

DEFINITION B12479 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION CB455341

VERSION CB455341.1 GI:29261723

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 631)

Smith, J.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-Mckown, C.G.,

Wray, J.E. and Keefe, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries

Unpublished

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

## TITLE

JOURNAL

COMMENT

Email: smith@emal.marc.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_alto option. Vector identified with  
 cross\_match v0.990329.  
 Plate: FQY8070 row: E column: 3  
 Seq primer: GTAATACGACTCATTATAGG.  
 Location/Qualifiers  
 1..631  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /issue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_id="MARC 680V"  
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
 library made with RNA pooled from multiple tissues  
 including liver, lung, hypothalamus, pituitary, and  
 placenta/endometrium."

BASE COUNT 99 a 174 c 193 g 164 t 1 others

Query Match 25.2%; Score 616; DB 14; Length 631;  
 Best Local Similarity 99.0%; Pred. No. 1.1e-95;  
 Matches 619; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1644 GAAACATATAGAGAGGCGCTGAGGAGCGCGCCGCTGCGTCCGAGCCGCTTCTC 1703  
 7 GAAACATATAGAGAGGCGCTGAGGAGCGCGCCGCTGCGTCCGAGCCGCTTCTC 66  
 1704 TGGTGAAGCCCGCCCTCCGACTGCGGCGCTCCCGCCCTGAGAGCGCTTCTC 1763  
 67 TGGTGAAGCCCGCCCTCCGACTGCGGCGCTCCCGCCCTGAGAGCGCTTCTC 126  
 1764 CTGTGCCAGGAGCGCCGGAAGATCTCGAATGCTCCCTGTGAGCTCTGTTTGT 1823  
 127 CTGTGCCAGGAGCGCCGGAAGATCTCGAATGCTCCCTGTGAGCTCTGTTTGT 186  
 1824 TTTTCTTCTGAGAGGAAGCTTGGAGAGCAGATCTGGACGACCTGTTTGTGAGT 1883  
 187 TTTTCTTCTGAGAGGAAGCTTGGAGAGCAGATCTGGACGACCTGTTTGTGAGT 246  
 1884 GCTACTCAGTACATAGCTTTTCTCAGTCCCTGAGTGTGTGTGTGTGTGTGTGT 1943  
 247 GCTACTCAGTACATAGCTTTTCTCAGTCCCTGAGTGTGTGTGTGTGTGTGTGT 306  
 1944 TGTGTGCGTGCAGT 2003  
 307 TGTGTGCGTGCAGT 366  
 2004 GTGTGTACTCGTGAAGAGAGCGGAGTGTGCGGAGCCCAAGGAGTGTGTGGAAGT 2063  
 367 GTGTGTACTCGTGAAGAGAGCGGAGTGTGCGGAGCCCAAGGAGTGTGTGGAAGT 426  
 2064 AGGGGCGCCCTGCTTATGCTGTTTGGGCTTGGAGAACTCAGAGGCGCACTTGG 2123  
 427 AGGGGCGCCCTGCTTATGCTGTTTGGGCTTGGAGAACTCAGAGGCGCACTTGN 486  
 2124 GGAACCTACGTGCGTCTGAGCGGTTTCCAGTATAGTATCCATCTTTTATCCACTC 2183  
 487 GGAACCTACGTGCGTCTGAGCGGTTTCCAGTATAGTATCCATCTTTTATCCACTC 546  
 2184 TGCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 606  
 547 TGCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 606  
 2244 CTGAAGTGTCCCAAGCAGCGGGG 2268  
 607 CTGAAGTGTCCCAAGCAGCGGGG 631

RESULT 6  
 CB467525  
 LOCUS 621 bp mRNA linear EST 26-MAR-2003

DEFINITION	7332727 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION	CB467525
VERSION	CB467525.1 GI:29273910
KEYWORDS	EST.
SOURCE	Bos taurus (cow)
ORGANISM	Bos taurus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
AUTHORS	1 (bases 1 to 621) Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keeler,J.W.
TITLE	A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL	Unpublished
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smithhemall.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_al option. Vector identified with cross match v0.990329. Plate: LAMB011 row: F column: 9 Seq primer: GTATTACGACCTCATRAGG. Location/Qualifiers 1..621
FEATURES	
Source	/organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="pooled" /lab_host="DH10B" /clone_id="MARC 6BOV" /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI; library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium." BASE COUNT 117 a 152 c 177 g 173 t 2 others ORIGIN
Query Match	25.1%; Score 612.2; DB 14; Length 621;
Best Local Similarity	99.2%; Pred. No. 5.2e-95;
Matches 614; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
QY	1798 CCGCTGTGACCTCCGTTGTTGTTTCTGAGAGAACTTTGAGAGACGAG 18557
Db	1 CCGCTGTGACCTCCGTTGTTGTTTCTGAGAGAACTTTGAGAGACGAG 60
QY	1858 CACGATCTGGACGACCACTGACCTGCTACTCACTCAGGTACATAGCTTTCTCAGCT 1917
Db	61 CACATCTGGAGGACCACTGACCTGCTACTCACTCAGGTACATAGCTTTCTCAGCT 120
QY	1918 GCCGTAGTGTGTCTGTGTGTAGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTCT 19777
Db	121 GCCGTAGTCT 180
QY	1978 GTATGTGCGTCTGT 20377
Db	181 GTATGTGCGTCTGT 240
QY	2038 AGCCCAAGGACGTGTTCCGAAGATGAGGGGCGCCCTGCTTATTTGCTGTTTGTGGGC 20977
Db	241 AGCCCAAGGACGTGTTCCGAAGATGAGGGGCGCCCTGCTTATTTGCTGTTTGTGGGC 300
QY	2098 TTGAGAACTGAGCAAGGCGACTGGGGGAACCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2157
Db	301 TTGAGAACTGAGCAAGGCGACTGGGGGAACCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY	2158 TAGATTAAGCCATCTTTGTATCACTCTGACATCACTCACTCACTCTGTATCACTAATAG 2217
Db	361 TAGATTAAGCCATCTTTGTATCACTCTGACATCACTCACTCACTCTGTATCACTAATAG 420
QY	2218 AAACCTTTGTGCGCTGCTGAGCAAGCTGATGCCAGGCAAGGCGGAGGACACAGAA 22777

Db	421	AAACTGTTGGTCCCTGCTGCTGGACCTGAACTGATCTCCCAAGCAGACGGGGAGACACGAA	480
Qy	2278	AAATGGGGCCCTCCCAAGGAGAGCTAGCTGTTCAAGTTCAGTTCAAGTCGCTCAAGTCGTCCG	2337
Db	481	AAATGGGGCCCTCCCAAGGAGAGCTAGCTGTTCAAGTTCAGTTCAAGTCGCTCAAGTCGTCCG	540
Qy	2338	ACCTTTGGGACCCCTTGAAATCCGAGGACCTCTGTAATACCTAAATCTTCACATTA	2397
Db	541	ACTCTTGGGACCCCTTGAAATCCGAGGACCTCTGTAATACCTAAATCTTCACATTA	600
Qy	2398	AAGCTTGCCCTGGAGGGA	2416
Db	601	AAGCTTGCCCTGGAGGGA	619
RESULT 7			
LOCUS	CB456735/c	611 bp	mRNA linear EST 26-MAR-2003
DEFINITION	CB456735		
ACCESSION	714023	MARC	6BOV Bos taurus cDNA 3', mRNA sequence.
VERSION	CB456735.1	GI:29263117	
KEYWORDS	EST.		
SOURCE	Bos taurus	(cow)	
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.		
AUTHORS	1 (bases 1 to 611)		
TITLE	Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keele,J.W. ESTs from pooled-tissue normalized libraries		
JOURNAL	A second set of bovine ESTs from pooled-tissue normalized libraries		
COMMENT	Unpublished		
	Contact: Smith TPL		
	USA, ARS, US Meat Animal Research Center		
	PO Box 166, Clay Center, NE 68933-0166, USA		
	Tel: 402 762 4366		
	Fax: 402 762 4390		
	Email: smith@email.marc.usda.gov		
	Single pass sequencing. Bases called with phred v0.020425.c and		
	trimmed with the aid of the trim_alo option. Vector identified with		
	cross_match v0.990329		
	Plate: FQY8070 row: E column: 3		
	Seq primer: TAGAAGGACAGCTGAG3.		
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	/lab_host="DH10B"		
	/clone_lib="MARC 6BOV"		
	/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;		
	library made with RNA pooled from multiple tissues		
	including liver, lung, hypothalamus, pituitary, and		
	placenta/endometrium."		
BASE COUNT	170 a	178 c	143 g
ORIGIN			120 t
Query Match	24.8%	Score 604.6;	DB 14; Length 611;
Best Local Similarity	99.3%;	Pred. No. 1e-93;	
Matches 607; Conservative	0;	Mismatches 4;	Indels 0; Gaps 0;
Qy	1818	GTTTTGTGTTTTTTTGGAGAGAAAGTCTGTGAGAGAGGACGATCTGGCAGCACGTA	1877
Db	611	GTTTTGTGTTTTTTTGGAGAGAAAGTCTGTGAGAGAGGACGATCTGGCAGCACGTA	552
Qy	1878	CTTGATCTACTACTCAGTGTATACATGATTTTCTCAGCTGCTCAAGTGTGTCTGTGT	1937
Db	551	CTTGATCTACTACTCAGTGTATACATGATTTTCTCAGCTGCTCAAGTGTGTCTGTGT	492
Qy	1938	GTAAGTGTGTCTGCGGACAGTGGGTGTGTTGTCTCTGTATGTGCGTCTGTGTGATG	1997

D	b		491	GTAGTGTGTCGTGGTGAGGCGCTGATGTTTGTCCTCTGTANTGGCGTCTGTGTANTG	432
O	y		1998	TGAGTGTCTGTACTCTCTGTGAGAGAGCCGAGTGTGCCCGAGACCAGGCACGTGGTCCG	2057
D	b		431	TGGAATTGTGTATCTCGTAGAGAGAGCCGAGTGTGCCCGAGACCAGGCACGTGGTCCG	372
O	y		2058	AAGATGAGGGGCGCCCTCCTCTTAATGGCTGTGTTTTGGGCTTGAGAACTACGAGAAGCG	2117
D	b		371	AAGATGAGGGGCGCCCTCCTCTTAATGGCTGTGTTTTGGGCTTGAGAACTACGAGAAGCG	312
O	y		2118	ACTTGGGGAACCTTACGTCTGTGGTCCCTGAGCCCGGTTTCCAGTAGATAGCAATCTTTGTAT	2177
D	b		311	ACTTGGGGAACCTTACGTCTGTGGTCCCTGAGCCCGGTTTCCAGTAGATAGCAATCTTTGTAT	252
O	y		2178	CCACTCTCACATCCACTCATCTCATCTGTGTACACTAATAGAAAACCTTTGGGCCCGCTG	2237
D	b		251	CCACTCTCACATCCACTCATCTCATCTGTGTACACTAATAGAAAACCTTTGGGCCCGCTG	192
O	y		2238	GACCAAGCTGAACCTGTCCCAGGACGCGGGGAGACAAGAAAAATGGGCGCTCCAGAGGA	2297
D	b		191	GACCAAGCTGAACCTGTCCCAGGACGCGGGGAGACAAGAAAAATGGGCGCTCCAGAGGA	132
O	y		2298	GCTAGCTGTTCAGTTCACTTTCAGTCCCTCAGTCGCTCCGATCCGATCTTTGGACCCCTGGAA	2357
D	b		131	GCTAGCTGTTCAGTTCACTTTCAGTCCCTCAGTCGCTCCGATCCGATCTTTGGACCCCTGGAA	72
O	y		2358	TCGCAAGGACCTTCTGTAAATACACTAAATCTTCCAATTAAGCTCTGCCCTGAGGAGAC	2417
D	b		71	TCGCAAGGACCTTCTGTAAATACACTAAATCTTCCAATTAAGCTCTGCCCTGAGGAGAC	12
O	y		2418	TGCTTAAAAAA 2428	
D	b		11	TGGCTGAAAAA 1	
R	E	S	U	L	T
RESULT 8					
CB430512			612 bp	mRNA	linear EST 25-MAR-2003
DEFINITION			606411 MARC BBOV Bos taurus cDNA 5', mRNA sequence.		
ACCESSION			CB430512		
VERSION			CB430512.1		GI:29206632
KEYWORDS			EST.		
SOURCE			Bos taurus (cow)		
ORGANISM			Bos taurus		
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. 1 (bases 1 to 612) Smith,T.P.L., Roberts,A.J., Becherkamp,S.E., Chitko-McKown,C.G., Wray,J.B. and Keeler,J.W. A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smitht@mail.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_al option. Vector identified with cross_match v0.990329. Plate: F0Y8024 row: F column: 24 Seq primer: GTAATACGATCAGCTATGAGG. Location/Qualifiers 1..612 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /feature_type="pooled" /lab_host="DH10B" /clone_lib="MARC BBOV" /note="Vector: pCDNA3.1, Site_1: EcoRI, Site_2: NotI, library made with RNA pooled from multiple tissues"		

[illegible]

PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390

Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
cross\_match v0.990329.  
Plate: F018024 row: F column: 18  
Seq primer: GTAAATGACATCTCATATGAGG.

## FEATURES

source

Location/Qualifiers  
1..591  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 6BOV"  
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
Library made with RNA pooled from multiple tissues  
including liver, lung, hypothalamus, pituitary, and  
placenta/endometrium."

BASE COUNT 80 a 168 c 211 g 132 t

ORIGIN

Query Match 24.0%; Score 584.6; DB 14; Length 591;  
Best Local Similarity 99.3%; Pred. No. 2.8e-90;  
Matches 587; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1426 TGGTGAAGGAGGCTGCGCGCTGGAGAGGAGTGTGCGCGCTGGAGCTGAGCG 1485  
1 TGGTGAAGGAGGCTGCGCGCTGGAGAGGAGTGTGCGCGCTGGAGCTGAGCG 60  
1486 AGCAGAGATGAGGCGCTGAGAGTGAAGACGAGCGCCACCTGCGCGAGCGAGTACA 1545  
61 AGCAGAGATGAGGCGCTGAGAGTGAAGACGAGCGCCACCTGCGCGAGCGAGTACA 120  
1546 GCATGCTGGCGCTGCG 1605  
121 GCATGCTGGCGCTGCG 180  
1606 GCCGGTCTCAGAGGACATGACCTGCTGGGTTGCTGGAGAAACATAGAGAGCGCTGG 1665  
181 GCCGGTCTCAGAGGACATGACCTGCTGGGTTGCTGGAGAAACATAGAGAGCGCTGG 240  
1666 GTGGCGCGCGCGCTGCGCGCTGCGAGCGCGCGCTTCTGTGGAAGCGCGCGCTCCGA 1725  
241 GTGGCGCGCGCGCTGCGCGCTGCGAGCGCGCGCTTCTCGGTGAAGCGCGCGCTCCGA 300  
1726 CTGGCGCGCTGCGCGCGCTGCGAGCGCGCTTCTGTGGAAGCGCGCGCTCCGA 1785  
301 CTGGCGCGCTGCGCGCGCTGCGAGCGCGCTTCTGTGGAAGCGCGCGCTCCGA 360  
1786 ATCTGGAGAGCGCTGCGCGCTGCGAGCGCGCTTCTGTGGAAGCGCGCGCTCCGA 1845  
361 ATCTGGAGAGCGCTGCGCGCTGCGAGCGCGCTTCTGTGGAAGCGCGCGCTCCGA 420  
1846 TGAAG 1905  
421 TGAAG 480  
1906 CTTTTCAGCTGCTGAGT 1965  
481 CTTTTCAGCTGCTGAGT 540  
1966 GTTGTGTCTGTATGT 2016  
541 GTTGTGTCTGTATGT 591

RESULT 10  
CB431220/c 586 bp mRNA linear EST 25-MAR-2003  
LOCUS  
DEFINITION 607179 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.

ACCESSION CB431220  
VERSION CB431220.1 GI:29208041  
KEYWORDS  
SOURCE

## ORIGIN

Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 586)

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contract: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
Plate: F018024 row: F column: 24  
Seq primer: TAGAAGCAGATCGAGC.

## FEATURES

source

Location/Qualifiers  
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/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 6BOV"  
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
Library made with RNA pooled from multiple tissues  
including liver, lung, hypothalamus, pituitary, and  
placenta/endometrium."

BASE COUNT 156 a 169 c 138 g 122 t 1 others

ORIGIN

Query Match 22.9%; Score 559.2; DB 14; Length 586;  
Best Local Similarity 97.6%; Pred. No. 6.4e-86;  
Matches 567; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

1837 AGAAGTCTTGAAG 1896  
586 AGAAGTCTTGAAG 527  
1897 TGTACATAGCTTTTCTCAGCTGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1956  
526 TGTACATAGCTTTTCTCAGCTGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 467  
1957 AGTGGGT 2016  
466 AGTGGGT 407  
2017 AGAAGCGGAGGTGTGCGCGGAGCCCAAGGCAATGTTGGAGAGAGAGAGAGAGAG 2076  
406 AGAAGCGGAGGTGTGCGCGGAGCCCAAGGCAATGTTGGAGAGAGAGAGAGAGAG 347  
2077 CTTATTCCTGTTTTTGTGGCTTGGAGAACTCAGCAAGGAGCACTTGGGAACTTACG 2136  
346 TTTATTCAGTTTGTGGCTTGGAGAACTCAGCAAGGAGCACTTGGGAACTTACG 287  
2137 GTCCCTGAGCGCGCTTGGAGAGTGAATGAAGCATCTTTGTATTCACCTGTGCACTC 2196  
286 GTCCCTGAGCGCGCTTGGAGAGTGAATGAAGCATCTTTGTATTCACCTGTGCACTC 227  
2197 ATCCACTGTGTACATATGAAGCACTTGTGCGCGGAGCCGAGCGAGCTGAAGTGTCCC 2256  
226 ATCCACTGTGTACATATGAAGCACTTGTGCGCGGAGCCGAGCGAGCTGAAGTGTCCC 167  
2257 AGGCAAGCGGAG 2316

Db 166 AGCAGCGGGGAGACAGAAAAATGGGGCTCCCAAGGAGCTAGTTCAGTTCACT 107  
 Qy 2317 TCAGTCGCTCAGTCTGTCCGACTCTTTGGCAGCCCTGTGAATCGAGGACTTCTGTAA 2376  
 Db 106 TCAGTCGCTCAGTCTGTCCGACTCTTTGGCAGCCCTGTGAATCGAGGACTTCTGTAA 47  
 Qy 2377 TACACTAAATCTTCAATTAAGCTGCGCCCTGAGGAGC 2417  
 Db 46 TACACTAAATCTTCAATTAAGCTGCGCTGTAGGAGC 6

## RESULT 11

AL559050

LOCUS 1042 bp mRNA linear EST 31-MAY-2003  
 DEFINITION Homo sapiens CDNA clone CS0DJ010YB05 5-PRIME, mRNA sequence.

ACCESSION AL559050  
 VERSION AL559050.2 GI:31283183

KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1042)  
 Li W.B., Gruber C., Jesse J., and Polayes D.  
 Full-length cDNA libraries and normalization

JOURNAL Unpublished  
 On Feb 15, 2001 this sequence version replaced gi:12904166.

COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 6595.r For more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0DJ010CA03QPLcluster=6595.r. Contact :  
 Peng Liang Email: fliang@life.com URL: <http://Fulllength.invitrogen.com/>  
 Faraday Avenue Genoscope sequence ID: CS0DJ010CA03QPL.

Location/Qualifiers  
 1. 1042

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DJ010YB05"  
 /cell\_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"  
 /cell\_line="JURKAT"  
 /clone\_1ib="Homo sapiens T CELLS (JURKAT CELL LINE) COT  
 10-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 247 a 278 c 277 g 236 t 4 others

## ORIGIN

Query Match 21.4%, Score 522; DB 9; Length 1042;  
 Best Local Similarity 72.9%; Pred. No. 1e-79;  
 Matches 726; Conservative 1; Mismatches 261; Indels 8; Gaps 4;

Qy 82 CGAGAGTCTCCGGGCTGTGGCCGCGAGGCTGGCCCTTCGGGTTTAAAGTCTCCCGGATT 141  
 Db 43 CGGAATTTCCCGGATGTGAGGCTCCAGTTCTGGCTTTGGGTTCAAGATCACTGGGACC 102  
 Qy 142 GGGCTGTG--TCCCGCCCTCACTCTCAACCTCCACCTCCCGAGCCGAGGCCCCGGCTC 198  
 Db 103 AGGCGGTGATCTTAAGCCGAGATCTCAACCTCACTGACCCCAAGGACTTGGAGC 162  
 Qy 199 CACTGGGCAATACCGAGACCGTGTGGTCTGTCATCTGCGGGCCGCACTGCCCC-AGC 257  
 Db 163 GTCCTGGAGACGAGTCCCGGAGAGCCCAAGACACTGCGGCTGCACACTGCGCTGAGC 222

Qy 258 CCTGATGGGGGATTGAGAGGCAACAGCTGGCCGAGATGAGGCTCCCGACCGTCTGC 317  
 Db 223 CCAATAGGGGAGTGAAGAGCCATAGCTGTCTGG-CATGGGCTCTCCACCGTCTGAC 281  
 Qy 318 CTGCTGTGCACTGTGTCTTCCAGCTCTGTGTGAGATGTATACCCCGAGGGTTTCA 377  
 Db 282 CTGCTGTGCACTGTGTCTTCCAGCTCTGTGTGAGATGTATACCCCGAGGGTTTAT 341  
 Qy 378 GGGCTGTCTCTACCCCGGAGACTGTGAGAGAGAGAGTCCCTTCCCGAAGAAA 437  
 Db 342 GAGCTGTCTCTACCTTGGAGAGAGAGAGATGTGTGTCTCCCAAGAAA 401  
 Qy 438 TATACCAACCGCAAAATAGACCATTTGTCTGACCAAGTGCACAAAGTACTTACTG 497  
 Db 402 TATATCAACCTCAAAATATTCATTTGCTGTACCAAGTGCACAAAGTACTTACTG 461  
 Qy 498 TACAATGACTGTGCGGGTCCAGGCGAGACCGAGCTGCAAGGTGTGTGCTCCCTG 557  
 Db 462 TACAATGACTGTGCGGGTCCAGGCGAGAGATACGAGCTGCAAGGTGTGTGAGAG 521  
 Qy 558 TACAATGACTGTGCGGGTCCAGGCGAGAGATACGAGCTGCAAGGTGTGTGAGAG 617  
 Db 522 TTCAACCGCTTCAAAACCACTTGAACACTGCTTCAAGTGTCTCAATGCGAAGAA 581  
 Qy 618 ATGTTCCAGTGTGAGATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 677  
 Db 582 ATGTTCCAGTGTGAGATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 641  
 Qy 678 AAGAACCAGTACCGGGAATTAATCTGGGGTGAATCTGGCTTCCGTTCTGAACTGAC 737  
 Db 642 AAGAACCAGTACCGGGAATTAATCTGGGGTGAATCTGGCTTCCGTTCTGAACTGAC 701  
 Qy 738 TGTCCCAATGAGCAAGTGAATTTCCCTTCCAGAGAGAGAGAGAGAGAGAGAGAG 797  
 Db 702 TGTCCCAATGAGCAAGTGAATTTCCCTTCCAGAGAGAGAGAGAGAGAGAGAGAG 761  
 Qy 798 CATATGGGCTCTTCTTAAAGGCGCAAGTGAATCTCTCTGATGATTTGAAGAA--C 854  
 Db 762 CATATGGGCTCTTCTTAAAGGCGCAAGTGAATCTCTCTGATGATTTGAAGAAAGC 821  
 Qy 855 AAGAGTGCAGAAAGTATGTTCCAAACCGCACTTCACTGTGAAGACTTCAAGACCA 914  
 Db 822 CTGAGTGCAGAAAGTATGTTCCAAACCGCACTTCACTGTGAAGACTTCAAGACCA 881  
 Qy 915 GGCATTAAGTACTTATTAACCCCTGTGTATTTCTTGGGCTTTTGGCTGCTTCCG 974  
 Db 882 GGCATTAAGTACTTATTAACCCCTGTGTATTTCTTGGGCTTTTGGCTGCTTCCG 941  
 Qy 975 TCTGTGCTTAGCATGTGCTACAGCGGTGGAAGCCAGACTTACTCATCATTTGC 1034  
 Db 942 TTCAATGTTTATGATATGCTTACCAAGGTGTGGAAGTCCAAAGCTTACTCATTT 1001  
 Qy 1035 GGGCAGTGCAGTCTGTGTAAGAGAGGGGAGCCAGA 1070  
 Db 1002 GGGRAATGCAGACCTGAAAGAGAGGGGAGCTTGA 1037

RESULT 12  
 CBS36686/c 519 bp mRNA linear EST 16-MAY-2003

LOCUS CBS36686  
 DEFINITION 771726 MARC BBOV Bov taurus cDNA 3', mRNA sequence.

ACCESSION CBS36686  
 VERSION CBS36686.1 GI:29404642

KEYWORDS EST.  
 SOURCE Bov taurus (cow)

ORGANISM Bov taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 519)  
 Smith T.P.L., Roberts A.J., Echtenkamp S.E., Chikio-Mckown C.G.,  
 Wray J.E. and Keefe J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries

TITLE

Qy 258 CCTGATGGGGGATTGAGAGGCAACAGCTGGCCGAGATGAGGCTCCCGACCGTCTGC 317  
 Db 223 CCAATAGGGGAGTGAAGAGCCATAGCTGTCTGG-CATGGGCTCTCCACCGTCTGAC 281  
 Qy 318 CTGCTGTGCACTGTGTCTTCCAGCTCTGTGTGAGATGTATACCCCGAGGGTTTCA 377  
 Db 282 CTGCTGTGCACTGTGTCTTCCAGCTCTGTGTGAGATGTATACCCCGAGGGTTTAT 341  
 Qy 378 GGGCTGTCTCTACCCCGGAGACTGTGAGAGAGAGAGTCCCTTCCCGAAGAAA 437  
 Db 342 GAGCTGTCTCTACCTTGGAGAGAGAGATGTGTGTCTCCCAAGAAA 401  
 Qy 438 TATACCAACCGCAAAATAGACCATTTGTCTGACCAAGTGCACAAAGTACTTACTG 497  
 Db 402 TATATCAACCTCAAAATATTCATTTGCTGTACCAAGTGCACAAAGTACTTACTG 461  
 Qy 498 TACAATGACTGTGCGGGTCCAGGCGAGACCGAGCTGCAAGGTGTGTGCTCCCTG 557  
 Db 462 TACAATGACTGTGCGGGTCCAGGCGAGAGATACGAGCTGCAAGGTGTGTGAGAG 521  
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 Db 522 TTCAACCGCTTCAAAACCACTTGAACACTGCTTCAAGTGTCTCAATGCGAAGAA 581  
 Qy 618 ATGTTCCAGTGTGAGATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 677  
 Db 582 ATGTTCCAGTGTGAGATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 641  
 Qy 678 AAGAACCAGTACCGGGAATTAATCTGGGGTGAATCTGGCTTCCGTTCTGAACTGAC 737  
 Db 642 AAGAACCAGTACCGGGAATTAATCTGGGGTGAATCTGGCTTCCGTTCTGAACTGAC 701  
 Qy 738 TGTCCCAATGAGCAAGTGAATTTCCCTTCCAGAGAGAGAGAGAGAGAGAGAGAG 797  
 Db 702 TGTCCCAATGAGCAAGTGAATTTCCCTTCCAGAGAGAGAGAGAGAGAGAGAGAG 761  
 Qy 798 CATATGGGCTCTTCTTAAAGGCGCAAGTGAATCTCTCTGATGATTTGAAGAA--C 854  
 Db 762 CATATGGGCTCTTCTTAAAGGCGCAAGTGAATCTCTCTGATGATTTGAAGAAAGC 821  
 Qy 855 AAGAGTGCAGAAAGTATGTTCCAAACCGCACTTCACTGTGAAGACTTCAAGACCA 914  
 Db 822 CTGAGTGCAGAAAGTATGTTCCAAACCGCACTTCACTGTGAAGACTTCAAGACCA 881  
 Qy 915 GGCATTAAGTACTTATTAACCCCTGTGTATTTCTTGGGCTTTTGGCTGCTTCCG 974  
 Db 882 GGCATTAAGTACTTATTAACCCCTGTGTATTTCTTGGGCTTTTGGCTGCTTCCG 941  
 Qy 975 TCTGTGCTTAGCATGTGCTACAGCGGTGGAAGCCAGACTTACTCATCATTTGC 1034  
 Db 942 TTCAATGTTTATGATATGCTTACCAAGGTGTGGAAGTCCAAAGCTTACTCATTT 1001  
 Qy 1035 GGGCAGTGCAGTCTGTGTAAGAGAGGGGAGCCAGA 1070  
 Db 1002 GGGRAATGCAGACCTGAAAGAGAGGGGAGCTTGA 1037



JOURNAL  
COMMENT  
Unpublished  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smitth@mail.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
cross match v0.990329.  
Plate: LAM8024 row: B column: 16  
Seq primer: TAGAAGCAGCAGTCGAGC.  
Location/Qualifiers  
1. 519  
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/db\_xref="taxon:9913"  
/issue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 6BOV"  
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
library made with RNA pooled from multiple tissues  
including liver, lung, hypothalamus, pituitary, and  
placenta/endometrium."

FEATURES  
source  
BASE COUNT 117 a 127 c 158 g 117 t  
ORIGIN

Query Match 21.1%; Score 514.2; DB 14; Length 519;  
Best Local Similarity 99.4%; Pred. No. 3.5e-78;  
Matches 516; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 643 GTGTAGTGGACCGGAGACACTGTGTGCGGCTGCAGAGAAACAGTCCGGAAATCTGGG 702  
DB 519 GTGTAGTGGACCGGAGACACTGTGTGCGGCTGCAGAGAAACAGTCCGGAAATCTGGG 460  
QY 703 GTGAACCTGGCTCCGGTGTGTGAATGCAAGCTCTGTCCCAATGGCACTGTAATATCC 762  
DB 459 GTGAACCTGGCTCCGGTGTGTGAATGCAAGCTCTGTCCCAATGGCACTGTAATATCC 400  
QY 763 CCTCCAGAGAGACAGGACACATCTGCCACTGCGATATGGCTTTCTTTAAAGGCG 822  
DB 399 CCTCCAGAGAGACAGGACACATCTGCCACTGCGATATGGCTTTCTTTAAAGGCG 340  
QY 823 CCAAGTGATCTCTGTGATGATTTGAAGAACAGAGTGGAGAGTTATATGCCAACC 882  
DB 339 CCAAGTGATCTCTGTGATGATTTGAAGAACAGAGTGGAGAGTTATATGCCAACC 280  
QY 883 GACCTTCACTGTGAAGACTCTCAGAGCCAGGACCTACAGTACTATTAACCCCTGTGA 942  
DB 279 GACCTTCACTGTGAAGACTCTCAGAGCCAGGACCTACAGTACTATTAACCCCTGTGA 220  
QY 943 TTGTCTTCGGGCTTTGCTGCGATCTTGGCTGTGTCTTGAAGATGGCTACAGC 1002  
DB 219 TTGTCTTCGGGCTTTGCTGCGATCTTGGCTGTGTCTTGAAGATGGCTACAGC 160  
QY 1003 GGTGAAGCCCAAGCTCTACTCATCATTTTCGCGGCACTGCACTCTGTAAAGAGGCGG 1062  
DB 159 GGTGAAGCCCAAGCTCTACTCATCATTTTCGCGGCACTGCACTCTGTAAAGAGGCGG 100  
QY 1063 AGCGAAGACTCTGTCTCCGCGCCGAGCTTCAACCCCAACCAACCACTGTGCTTCACT 1122  
DB 99 AGCGAAGACTCTGTCTCCGCGCCGAGCTTCAACCCCAACCAACCACTGTGCTTCACT 40  
QY 1123 CCACCCCAAGTTCAGTCTGTCTCCATTCGCCCTTACA 1161  
DB 39 CCACCCCAAGTTCAGTCTGTCTCCATTCGCCCTTAAA 1

RESULT 13  
CD288290 545 bp mRNA linear EST 27-MAY-2003  
LOCUS CD288290  
DEFINITION 3\_P15.abd POR14 (Day\_14\_pregnant\_ovine\_endometrium) Ovis aries cDNA  
, mRNA sequence.

ACCESSION CD288290  
VERSION CD288290.1 GI:31086333  
KEYWORDS EST.  
SOURCE Ovis aries (sheep)  
ORGANISM Ovis aries

REFERENCE  
AUTHORS Gray,C.A., Adelson,D.L. and Spencer,T.E.  
TITLE Ovine ESTs  
JOURNAL Unpublished  
COMMENT Contact: Thomas E. Spencer  
Center for Animal Biotechnology and Genomics  
Texas A&M University  
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,  
USA  
Tel: 9798454896  
Fax: 9798622662  
Email: tepencer@ansc.tamu.edu.  
Location/Qualifiers  
1. 545  
/organism="Ovis aries"  
/mol\_type="mRNA"  
/db\_xref="taxon:9940"  
/sex="Female"  
/issue\_type="endometrium"  
/day\_stage="Day 14 pregnant"  
/clone\_lib="POR14 (Day 14 pregnant ovine endometrium)"  
/note="Organ: uterus; Vector: Triplex2; Site 1: EcoRI;  
Site 2: XhoI; Non-normalized library, sequenced 5' with  
Triplex2 primer (CTCCGAGATGTGACGCG). Library constructed  
by Clontech with total RNA extracted using the Trizol  
method and pooled from 5 females."

FEATURES  
source  
BASE COUNT 109 a 165 c 167 g 104 t  
ORIGIN

Query Match 21.0%; Score 513; DB 14; Length 545;  
Best Local Similarity 96.3%; Pred. No. 5.4e-78;  
Matches 525; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 187 AGCCCGCGGCTCCACTGGGCAATACGAGACCGTGTCTGTACTGTCCGGGCGGCC 246  
DB 1 AGCCCGCGGCTCCACTGGGCAATACGAGACCGTGTCTGTACTGTCCGGGCGGCC 60  
QY 247 ACTGCCCGAGCCCGATGGGGGATTTGAGGGCCACAGCTGGCGGAGACATGGGCTCCCA 306  
DB 61 ACTGCCCGAGCCCGATGGGGGATTTGAGGGCCACAGCTGGCGGAGACATGGGCTCCCA 120  
QY 307 CCGTGCTGGCTGCTCTGCTGCACTGGTGTCTTCAGCTCTGTGGCAGATGTATACCCG 366  
DB 121 CCGTGCTGGCTGCTCTGCTGCACTGGTGTCTTCAGCTCTGTGGCAGATGTATACCCG 180  
QY 367 CAGGGGTTCAAGGGGCTGTCTCAACCCCGGGGACCTGGAGAGAGAGAGTCCCTGTC 426  
DB 181 CAGGGGTTCAAGGGGCTGTCTCAACCCCGGGGACCTGGAGAGAGAGAGTCCCTGTC 240  
QY 427 CCCAAGGAATAATTAACACCCCGCAAAATAGCACTTTGTGTGACCAAGTGGCCAAAG 486  
DB 241 CCCAAGGAATAATTAACACCCCGCAAAATAGCACTTTGTGTGACCAAGTGGCCAAAG 300  
QY 487 GTACTTATCTGTACATGACTGTCCGGGCTCAGGGGAGACACCGAGCTGACGGGTGTGTG 546  
DB 301 GTACTTATCTGTACATGACTGTCCGGGCTCAGGGGAGACACCGAGCTGACGGGTGTGTG 360  
QY 547 CCCTGTGACCTTACACTGCTGTGGAGAACATTTCAACGATGCTTGAAGTCTTCACGT 606  
DB 361 CCCTGTGACCTTACACTGCTGTGGAGAACATTTCAACGATGCTTGAAGTCTTCACGT 420  
QY 607 GCGGGAAGAAATTTCCAGGTGAGATTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 666  
DB 421 GCGGGAAGAAATTTCCAGGTGAGATTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480

QY 667 GCGGTCGAGAGAACGAGTACCGGGAATCTGGGGTGAACAGTGGCTTCGGGTCTGCA 726  
 DB 461 GTGGCTGCAAGAGAACGAGTACCGGGAATCTGGGGGAGAACTGGCTTCGGGTCTGCA 540  
 QY 727 ACTGC 731  
 DB 541 ACTGC 545  
 RESULT 14  
 BX377601 1096 bp mRNA linear EST 08-MAY-2003  
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 DEFINITION clone CS0D1008Yp21 5-PRIME, mRNA sequence.  
 ACCESSION BX377601  
 VERSION BX377601.1 GI:30435085  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 1096)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 6595.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0D1008CH10Pic1cluster=6595.r. Contact :  
 Peng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/invitrogen Corporation 1600  
 Paraday Avenue Genoscope sequence ID : CS0D1008CH10P1.  
 Location/Qualifiers  
 1..1096  
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 /note="1st strand cDNA was primed with a NotI-oligo (dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
 BASE COUNT 258 a 303 c 284 g 248 t 3 others  
 ORIGIN  
 Query Match 21.0%; Score 511.8; DB 13; Length 1096;  
 Best Local Similarity 73.2%; Pred. No. 5,6e-78;  
 Matches 708; Conservative 2; Mismatches 249; Indels 8; Gaps 4;  
 QY 111 CTGGGCTTCGGGGTTGAGTCTCCGAGTGGGGTGG---TCCCGCCCGAGTCTCA 167  
 DB 55 CTGGGCTTCGGGGTTGAGTCTCCGAGTGGGGTGG---TCCCGCCCGAGTCTCA 114  
 QY 168 CCTTCACCTCCCGAGCCCGAGGCGCGCTCCATCGGCGATACGAGAGACCGTGTGCT 227  
 DB 115 CCTTCACCTCCCGAGCCCGAGGCGCGCTCCATCGGCGATACGAGAGACCGTGTGCT 174  
 QY 228 GTCACTGTGCGGGCGCGCGCTCCCGAGGCGCGCTCCATCGGCGATACGAGAGACCGTGTGCT 286  
 DB 175 CCAGACACGCGCGCTCCCGAGGCGCGCTCCATCGGCGATACGAGAGACCGTGTGCT 234  
 QY 287 GCCGAGATGGGGCTCCCGAGGCGCGCTCCCGAGGCGCGCTCCATCGGCGATACGAGAGACCGTGTGCT 346  
 DB 235 TCTGG-CATGGGCTTCACCGCGGCTCGACCTGTGCTGCGACCTGGGTCTCTGGAGCT 293  
 QY 347 GTTGGCAGATGTGTAACCCCGAGGCGGTTCAAGGCGGCTGCTCCCTCAACCCCGGAGACTTGA 406

DB 294 GTTGGGGAATATACCCCTTACGAGGATATTGACGTGCTCCCTCACTAGGAGACAGGA 353  
 QY 407 GAAGAGAGAGATCCCTGTCTCCCAAGAAATATTAACCAACCCGCAAAATAGACCATTTG 466  
 DB 354 GAAGAGAGATATGTGTGTGTCTCCCAAGAAATATTAACCAACCCGCAAAATAGACCATTTG 413  
 QY 467 CTGCACCAAGTCCCAAAAGTATCTATCTATCAATATGATCTGTGCTCCAGGCGAGA 526  
 DB 414 CTGTACCAAGTCCCAAAAGTATCTATCTATCAATATGATCTGTGCTCCAGGCGAGA 473  
 QY 527 CACGAGCTGACGGGTTGTGCGCCCTGAGCACTTACCTGCTTGGAGAACATCTCAGAG 586  
 DB 474 TACGAGCTGACGGGTTGTGCGCCCTGAGCACTTACCTGCTTGGAGAACATCTCAGAG 533  
 QY 587 ATGCTTGAAGTCTTCCAGGTGCGGAGCAAAATGTTCCAGGTGAGATTTGCGCTGTGT 646  
 DB 534 CTGCTTGAAGTCTTCCAGGTGCGGAGCAAAATGTTCCAGGTGAGATTTGCGCTGTGT 593  
 QY 647 AGTGACCTGGAGCACTGTGTGCGGCTGAGAGAAACCAATACCGGAAATCTGGAGTGA 706  
 DB 594 AGTGACCTGGAGCACTGTGTGCGGCTGAGAGAAACCAATACCGGCAATTTGAGAGTGA 653  
 QY 707 AACTGCTTCCGGTGTGTAAGTCAAGCTGCTGCTCCCAATGAGCAAGTAAATATCCCTG 766  
 DB 654 AACTCTTCCAGTGTGTAAGTCAAGCTGCTGCTCCCAATGAGCAAGTAAATATCCCTG 713  
 QY 767 CCAGAGAGACAGAGACCAATCTGCACTGCACTGATGAGGCTTCTTTTAAAGCGCCGA 826  
 DB 714 CCAGAGAGACAGAGACCAATCTGCACTGCACTGATGAGGCTTCTTTTAAAGAGAAAGCA 773  
 QY 827 GTGCATCTCTCTGTATGTTTATAGAA---CAAGAGTGCAGAAAGTATATCCAAACCG 883  
 DB 774 GTGCTCTCTGTATGTTTATAGAAAGTATATCCAAACCGTATGCTTCAACCA 833  
 QY 884 AACTTCAACTGTATTAAGTCACTGCACTGCACTGATGAGGCTTCTTTTAAAGCGCCGA 943  
 DB 834 GATTGAGAAATTTAAGGCACTGAGCACTGAGCACTGAGCACTGAGTGTGCTTGTGCTAT 893  
 QY 944 TGTCTTGGGCTTGTGCTGAGTCTTGTGCTGCTGCTGCTTGTGCTTGTGCTTGTGCT 1003  
 DB 894 TGTCTTGGGCTTGTGCTGAGTCTTGTGCTGCTGCTGCTTGTGCTTGTGCTTGTGCT 953  
 QY 1004 GTGAGCGCCAGGCTATCTTCCATCTTGGGGGAGTCACTGTGTAAGAGGGGGA 1063  
 DB 954 GTGAGCGCCAGGCTATCTTCCATCTTGGGGGAGTCACTGTGTAAGAGGGGGA 1013  
 QY 1064 GCCAGAA 1070  
 DB 1014 GCTTGA 1020  
 RESULT 15  
 B1898540 502 bp mRNA linear EST 17-OCT-2001  
 LOCUS B1898540  
 DEFINITION 479493 MARC 2Bov Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION B1898540  
 VERSION B1898540.1 GI:16203989  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 502)  
 AUTHORS Smith, T.P.L., Grose, W.M., Preking, B.A., Roberts, A.J., Stone, R.T.,  
 Casar, E., Wray, J.E., White, J., Cho, J., Fahrnenkrug, S.C., Bennett,  
 G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chiklo-McKown, C.G.,  
 Pertea, G., Holt, I., Karaycheva, S., Liang, F., Quackenbush, J., and  
 Keefe, J.W.  
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle  
 JOURNAL Genome Res. 11 (4), 626-630 (2001)



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 13, 2003, 06:55:24 ; Search time 47 Seconds

(without alignments)  
1590.643 Million cell updates/sec

Title: US-09-970-532-2

Sequence: 1 MGLPTVGLLLPLVLPALLA.....NIEBALGGAARLASERPLW 471

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	2603	100.0	471	AAE25816
2	2603	100.0	471	ABE58169
3	1517	58.3	455	11 ABG74751
4	1517	58.3	455	11 ABG74755
5	1517	58.3	455	12 AAR10986
6	1517	58.3	455	14 AAR42059
7	1517	58.3	455	16 AAR75084
8	1517	58.3	455	20 AAY30934
9	1517	58.3	455	21 AAB36266

10	1517	58.3	455	21 AAB37800	Human tumour necro
11	1517	58.3	455	21 AAB26984	Human TNFR 1. Hom
12	1517	58.3	455	21 AAB23446	Human tumour necro
13	1517	58.3	455	21 AAB01336	TNF-R1 death recep
14	1517	58.3	455	22 AAB66817	Human TNFIP-associ
15	1517	58.3	455	22 AAB36697	Human tumour necro
16	1517	58.3	455	22 AAB37677	Human 30 kDa TNF 1
17	1517	58.3	455	23 AAB54789	Human COPD-related
18	1517	58.3	455	23 AAO22286	TNFR1 expression m
19	1517	58.3	455	23 ABB81649	Human tumour necro
20	1517	58.3	455	23 AAU75064	Human tumour necro
21	1514	58.2	455	12 AAR11082	Human 55kD TNF-bin
22	1511	58.0	455	13 AAR20787	TNF-alpha binding
23	1508	57.9	455	11 AAR07451	Human Tumour Necro
24	1508	57.9	455	14 AAR42197	p55 Tumour necrosi
25	1505	57.8	455	14 AAR51034	Mutant p55 tumour
26	1500.5	57.6	909	19 AAM64485	Human Fas protein.
27	1496	57.5	453	22 AAB50895	Human TNFR 1. Hom
28	1494	57.4	455	12 AAR12550	Type I TNF recepto
29	1492	57.3	455	13 AAR24000	TNF-alpha 55kd rec
30	1491	57.3	443	14 AAB51033	Mutant p55 tumour
31	1486	55.9	433	14 AAR51032	Mutant p55 tumour
32	1325.5	50.9	461	11 ABG74754	Rat TNF-R protein
33	1319.5	50.7	461	11 AAR07450	Rat Tumour Necrosi
34	1319	50.7	454	23 AAO22289	TNFR1 expression m
35	1178	45.3	371	11 ABG74753	Human TNF-RP prote
36	1178	45.3	371	11 AAR07449	Tumour Necrosis fa
37	1072	41.2	181	23 AAE25817	Tumour Necrosis fa
38	1072	41.2	280	22 ABB98170	Bovine tumour necr
39	1019	39.1	280	22 AAB66979	Soluble bovine tum
40	834.5	32.1	233	24 ABB99540	Tnfr1 protein. Un
41	833	32.0	444	24 ABB37098	Amino acid sequenc
42	832.5	32.0	211	20 AAM89225	Concatameric immun
43	832.5	32.0	311	20 AAM89229	Tumour necrosis fa
44	832.5	32.0	366	20 AAM89228	Tumour necrosis fa
45	832.5	32.0	397	20 AAM89227	Tumour necrosis fa

#### ALIGNMENTS

RESULT 1	AAE25816	standard; Protein: 471 AA.
ID	AAE25816	
AC	AAE25816	
XX		
DT	15-NOV-2002	(first entry)
XX		
DE	Bovine tumour necrosis factor receptor-I (TNF-R1).	
XX		
KM	Bovine; cattle; coliform masticis; inflammatory disease; receptor;	
KM	tumour necrosis factor receptor-I; TNF-R1; antiinflammatory.	
XX		
OS	Bos taurus.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..29
FT	Protein	/label= Signal_peptide
FT	Domain	/note= "Mature bovine TNF-R1"
FT	Domain	30..210
FT	Modified-site	/note= "Extracellular domain"
FT	Modified-site	54..56
FT	Modified-site	/note= "N-linked glycosylation site"
FT	Modified-site	145..147
FT	Modified-site	/note= "N-linked glycosylation site"
FT	Modified-site	151..153
FT	Domain	/note= "N-linked glycosylation site"
FT	Domain	211..235
FT	Domain	/note= "Transmembrane domain"
XX		
PN	US6406907-B1.	

XX 18-JUN-2002.  
 PD 25-FEB-2000; 2000US-0513007.  
 PF 26-FEB-1999; 99US-122156P.  
 XX (IOWA ) UNIV IOWA STATE RES FOUND INC.  
 XX (USDA ) US SEC OF AGRIC.  
 PA Taylor MJ, Kehrli ME, Lee E;  
 XX MPI; 2002-588816/63.  
 XX N-PSDB; AAD42477.  
 XX Novel nucleic acid molecule encoding bovine tumor necrosis factor  
 PT receptor-I which is a potent inhibitor of tumor necrosis factor-alpha  
 XX useful for treating coliform mastitis or other inflammatory disease in  
 XX cattle  
 PS Claim 8; Column 17-20; 16pp; English.  
 CC The invention relates to an isolated nucleic acid encoding a polypeptide  
 CC that binds bovine tumor necrosis factor (TNF). The invention is useful  
 CC for expressing bovine TNF-R1 or soluble bovine TNF-R1 which is useful as  
 CC an inhibitor of TNF in cattle suffering from coliform mastitis or other  
 CC inflammatory disease. The nucleic acids and polypeptide or their  
 CC fragments are useful for treating mastitis. The present sequence is  
 CC bovine tumor necrosis factor receptor-I (TNF-R1).  
 CC  
 XX Sequence 471 AA;  
 SQ  
 Query Match 100.0%; Score 2603; DB 23; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-170; Mismatches 0; Indels 0; Gaps 0;  
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKESPCPOGKYNHPONSTICT 60  
 DB 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKESPCPOGKYNHPONSTICT 60  
 QY KCHKGTLYNDPCPGRDTCVCAPGTYTALENHLRRLCSRCRDEMFVEISPCVVD 120  
 DB 61 KCHKGTLYNDPCPGRDTCVCAPGTYTALENHLRRLCSRCRDEMFVEISPCVVD 120  
 QY 121 RDTVCGCRKNQRYREYMGEGFRCLNCSLCPNGTVNI PCQERODTICHGMGFLKGAKCI 180  
 DB 121 RDTVCGCRKNQRYREYMGEGFRCLNCSLCPNGTVNI PCQERODTICHGMGFLKGAKCI 180  
 QY 181 SCHDCKNKECEKLCPTPSTGKOSODPGTTVLLPLVIVFGCLASFASVVLACRYQRMKP 240  
 DB 181 SCHDCKNKECEKLCPTPSTGKOSODPGTTVLLPLVIVFGCLASFASVVLACRYQRMKP 240  
 QY 241 KLYSIICGOSTLVKGEPELVLPAPGFNPPTTICSSSTPSSSPVSIPIPTISCDRNFAGAV 300  
 DB 241 KLYSIICGOSTLVKGEPELVLPAPGFNPPTTICSSSTPSSSPVSIPIPTISCDRNFAGAV 300  
 QY 301 ASPSSETAPPHLKAGPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLCCTPVQKWEASA 360  
 DB 301 ASPSSETAPPHLKAGPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLCCTPVQKWEASA 360  
 QY 361 PSAPPOLADADPATIYAVVDGVPSPRWKELVRLGLSEHEIRLELNGRHLREAOYSML 420  
 DB 361 PSAPPOLADADPATIYAVVDGVPSPRWKELVRLGLSEHEIRLELNGRHLREAOYSML 420  
 QY 421 AAMRRRTPRREATLELGRVLRMDMLGCLENIEEALGGAALASEPRLLM 471  
 DB 421 AAMRRRTPRREATLELGRVLRMDMLGCLENIEEALGGAALASEPRLLM 471

RESULT 2  
 ABB98169  
 ID ABB98169 standard; Protein; 471 AA.  
 XX

AC ABB98169;  
 XX 05-NOV-2002 (first entry)  
 DT Bovine tumour necrosis factor receptor-I.  
 XX Bovine tumour necrosis factor receptor-I.  
 DE Bovine; tumour necrosis factor receptor-I; TNF-R1; antiinflammatory;  
 XX TNF cytotoxicity; mastitis; tumour necrosis factor-alpha; TNF-alpha;  
 KW monoclonal antibody BC9; TNF-beta.  
 XX Boe taurus.  
 XX US2002076765-A1.  
 XX 20-JUN-2002.  
 PD 03-OCT-2001; 2001US-0970532.  
 XX 26-FEB-1999; 99US-122156P.  
 XX 25-FEB-2000; 2000US-0513007.  
 XX (IOWA ) UNIV IOWA STATE RES FOUND INC.  
 PA Taylor MJ, Kehrli ME, Lee E, Mwangi S;  
 XX MPI; 2002-557247/59.  
 XX N-PSDB; ABQ79378.  
 DR New isolated, soluble, bovine tumour necrosis factor receptor I, useful  
 PT for inhibiting tumour necrosis factor cytotoxicity for treating  
 PT mastitis, is a better inhibitor of tumour necrosis factor compared to  
 PT monoclonal antibody BC9 -  
 XX  
 PS Claim 8; Fig 1; 17pp; English.  
 CC The invention relates to an isolated nucleic acid encoding bovine tumour  
 CC necrosis factor receptor-I (TNF-R1). The activity of polynucleotides of  
 CC the invention may be described as antiinflammatory. Polypeptides of the  
 CC invention are useful for inhibiting TNF cytotoxicity in a bovine. This is  
 CC useful for treating mastitis and other inflammatory disease. Soluble  
 CC bovine TNF-R1 is a better inhibitor of bovine TNF-alpha than monoclonal  
 CC antibody BC9 (an antibody directed towards TNF-alpha), and can bind both  
 CC TNF-alpha and TNF-beta. The current sequence represents bovine tumour  
 CC necrosis factor receptor-I.  
 CC  
 XX Sequence 471 AA;  
 SQ  
 Query Match 100.0%; Score 2603; DB 23; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-170; Mismatches 0; Indels 0; Gaps 0;  
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKESPCPOGKYNHPONSTICT 60  
 DB 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKESPCPOGKYNHPONSTICT 60  
 QY 61 KCHKGTLYNDPCPGRDTCVCAPGTYTALENHLRRLCSRCRDEMFVEISPCVVD 120  
 DB 61 KCHKGTLYNDPCPGRDTCVCAPGTYTALENHLRRLCSRCRDEMFVEISPCVVD 120  
 QY 121 RDTVCGCRKNQRYREYMGEGFRCLNCSLCPNGTVNI PCQERODTICHGMGFLKGAKCI 180  
 DB 121 RDTVCGCRKNQRYREYMGEGFRCLNCSLCPNGTVNI PCQERODTICHGMGFLKGAKCI 180  
 QY 181 SCHDCKNKECEKLCPTPSTGKOSODPGTTVLLPLVIVFGCLASFASVVLACRYQRMKP 240  
 DB 181 SCHDCKNKECEKLCPTPSTGKOSODPGTTVLLPLVIVFGCLASFASVVLACRYQRMKP 240  
 QY 241 KLYSIICGOSTLVKGEPELVLPAPGFNPPTTICSSSTPSSSPVSIPIPTISCDRNFAGAV 300  
 DB 241 KLYSIICGOSTLVKGEPELVLPAPGFNPPTTICSSSTPSSSPVSIPIPTISCDRNFAGAV 300  
 QY 301 ASPSSETAPPHLKAGPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLCCTPVQKWEASA 360  
 DB 301 ASPSSETAPPHLKAGPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLCCTPVQKWEASA 360

Db	301	ASPSSETPAPHLKAGPILPCGPASTHLCCTGPAPASTHLCCTPGPASTHLCCTPVQKMEASA	360
Qy	361	PSAPDQADADDPATLYAVVDGVPSPRWKELVRLGLSGSEHIEIRLELNGHRLREAOYSML	420
Db	361	PSAPDQADADDPATLYAVVDGVPSPRWKELVRLGLSGSEHIEIRLELNGHRLREAOYSML	420
Qy	421	AAMRRRTPRREATLELIGRVLRQMDLGLCLENIEEALGSAARLASBPRLM	471
Db	421	AAMRRRTPRREATLELIGRVLRQMDLGLCLENIEEALGSAARLASBPRLM	471
RESULT 3			
		ABG74751 standard; Protein: 455 AA.	
		ABG74751	
XX	XX	ABG74751;	
AC	AC		
XX	XX	14-MAY-2003 (first entry)	
DT	DT		
XX	XX	Human TNF receptor protein.	
DE	DE		
KM	KM	TNF; human; tumour necrosis factor; tumour necrosis factor receptor;	
KM	KM	TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.	
XX	XX		
OS	OS	Homo sapiens.	
PN	PN	EPJ93438-A.	
XX	XX	24-OCT-1990.	
PD	PD		
XX	XX	06-APR-1990; 90EP-0106624.	
PF	PF		
XX	XX	21-APR-1989; 89DE-3913101.	
PR	PR	21-JUN-1989; 89DE-3920282.	
XX	XX	(BOEH ) BOEHRINGER INGELHEIM INT GMBH.	
PA	PA	(SYND ) SYNERGEN INC.	
XX	XX		
PI	PI	Hauptmann R, Himmel A, Maurer-Fogy I, Stralowa C;	
XX	XX	WPI; 1990-321987/43.	
DR	DR		
XX	XX	DNA encoding TNF binding protein and TNF-receptor - used in tumour	
PT	PT	treatment and to understand mechanisms to TNF action	
XX	XX		
PS	PS	Claim 22; Page 34; 51pp; German.	
CC	CC	This invention describes novel polynucleotide sequences encoding tumour	
CC	CC	necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).	
CC	CC	The products of the invention are useful in pharmaceutical compositions	
CC	CC	for prophylaxis or treatment of human tumours and to understand the	
CC	CC	mechanisms of TNF action. This sequence represents the TNF receptor	
CC	CC	described in the disclosure of the invention.	
XX	XX		
SQ	SQ	Sequence 455 AA:	
Qy	Query Match	58.3%; Score 1517; DB 11; Length 455;	
Db	Best Local Similarity	62.9%; Pred. No. 1.4e-95;	
Db	Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;		
Qy	1	MGLPLVPGLLPLVLVPALLADVPYRPGVQGLVHHPDLEKRESPCQGRKYNHQNSTICT	60
Db	1	MGLSTVPDLPLPLVLELVLVGIYPGSGVIGLVPLHLDREKRDVCPQGRKYNHQNSTICT	60
Qy	61	KHKRGTYLYNDPRGPGDTCRVCAPGTVALENHLRCLSGCRDEMFOVEISPCVVD	120
Db	61	KHKRGTYLYNDPRGPGDTCRVCAPGTVALENHLRCLSGCRDEMFOVEISPCVVD	120
Qy	121	RDVCGCRNQYREYWGEGTGRFLNCLSLCPNGTVNIPQGRDITICHMGFFLKGAKCI	180
Db	121	RDVCGCRNQYRHYWSENLFQCFNCSICLNGTVHLSCEQKQNTVCTGAGFFLRENECV	180
Qy	181	SCHDCKNK-ECEKLCPTRPSTGKSDSDPDTYLLPLVLYVFGICLASFASVLAACRYQRWK	239

Db	181	SCSNCKSLSEETKCLPQIEWVKGTEDSGTVLLPLVIFCLCLSLFLGLMYRQRMK	240
Oy	240	PKLYSIICGGSTLVKEGEPE-----LVPAAGFNP-----TTTIFSSITPSSPVSIPRY	290
Db	241	SKLVSIVCGKSTPKKEGELEGTITTKPLAPNPSFSPDGFPTLGLFSPVSSSTFTSSSTYT	300
Oy	291	SCDSNFGAVASPSESTAPPHLKXGPILPGPASTHLCCTPGPASTHLCCTGPPASTHLC	350
Db	301	PGDCPNF---AAPREVAAPPIQGADPIL-----ATL-----ASDPF	335
Oy	351	TPVQKWEASAPSDOLADADPATLVAVVDGVPSPRWKELVRLGLSEHIERLENGR	410
Db	336	NPLQKWEDSA-HKQSLDTPDPAVLVAVENVPPLRWKEFVRLQLGSDHEIDRLLELQGR	394
Oy	411	HLRPAQVSMLAAMRRPFRPRPATTELLGRVTRDMDLGLCLENIEBALGGAARLASERPLL	470
Db	395	CLRAQVSMLATWRRRTPRREATLELLGRVLRDMDLGLCLEDIEBALCGPALPPAPSL	454
RESULT 4			
ABG74755	ID	ABG74755 standard; Protein; 455 AA.	
AC	ABG74755;		
XX	14-MAY-2003	(first entry)	
XX	Human TNF-R protein huTNF-R.		
XX	TNF, human; tumour necrosis factor; tumour necrosis factor receptor;		
XX	TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.		
XX	Homo sapiens.		
XX	EP393438-A.		
XX	24-OCT-1990.		
XX	06-APR-1990;	90EP-0106624.	
XX	21-APR-1989;	89DE-3913101.	
XX	21-JUN-1989;	89DE-3920262.	
XX	(BOEH ) BOEHRINGER INGENHEIM INT GMBH.		
XX	(SYND ) SYNERGEN INC.		
XX	Hauptmann R, Himmler A, Maurer-Fogy I, Stralow C;		
XX	WPI, 1990-321987/43.		
XX	DR N-PSDB; AB077487.		
XX	DNA encoding TNF binding protein and TNF- receptor - used in tumour		
XX	treatment and to understand mechanisms to TNF action		
XX	Example 9; Fig 9; 51pp; German.		
XX	This invention describes novel polynucleotide sequences encoding tumour		
XX	necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).		
XX	The products of the invention are useful in pharmaceutical compositions		
XX	for prophylaxis or treatment of human tumours and to understand the		
XX	mechanisms of TNF action. This sequence represents the huma TNF-R,		
XX	CC huTNF-R described in the disclosure of the invention.		
XX	SQ	Sequence	455 AA;
Oy	Query Match	58.3%;	Score 1517; DB 11; Length 455;
Db	Best Local Similarity	62.9%;	Pred. No. 1.4e-95;
Db	Matches 302; Conservative 38;	Mismatches 104;	Indels 36; Gaps 7
Db	1 MGLPTVPGILLPLVLPALADAVPAGVQGLVHPGDLKGRSPCPDQKYNHPQNSTICT	60	
Db	1 MGLSTVPDLPLVLVLLELLVGVISGVIGLVPHLGRKRDSDVCPQGXKTIHPQNNISICT	60	

QY 61 KCHKGTLYNDGPGRDPTDCRCVACPTTALLENHRLCLSCRCRDEMFOVEISPCVVD 120  
 DB 61 KCHKGTLYNDGPGRDPTDCRCVACPTTALLENHRLCLSCRCRDEMFOVEISPCVVD 120  
 QY 121 RDTVCGCRKQRYREYWGSTGFRCLNCSLCPNGTVNI PCOERODTICHCHMGFFLKAKCI 180  
 DB 121 RDTVCGCRKQRYREYWGSTGFRCLNCSLCPNGTVNI PCOERODTICHCHMGFFLKAKCI 180  
 QY 181 SCHDCRKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLASFAVYLACRYQRWK 239  
 DB 181 SCHDCRKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLASFAVYLACRYQRWK 239  
 QY 240 PKYXIIICGOSTLVKEGPE-----LVVAPGPNP-----TTTICFSTSPSSSPVSIIPPYI 290  
 DB 240 PKYXIIICGOSTLVKEGPE-----LVVAPGPNP-----TTTICFSTSPSSSPVSIIPPYI 290  
 QY 291 SCDSNFGAVASPSSETAPRHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350  
 DB 291 SCDSNFGAVASPSSETAPRHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350  
 QY 301 PGDCPNF---AARREVAPPYOGADPIL-----ATML-----ASDP1P 335  
 DB 301 PGDCPNF---AARREVAPPYOGADPIL-----ATML-----ASDP1P 335  
 QY 351 TPVQKMEASAPSPDOLADADPATLYAVVDGVPSPRWKELVRRLGLSEHEIERLEENGR 410  
 DB 351 TPVQKMEASAPSPDOLADADPATLYAVVDGVPSPRWKELVRRLGLSEHEIERLEENGR 410  
 QY 336 NPLQKMEASA-HKQSLDTPDTPATLYAVVENVPPLRMKEFVRRLGLSDHEIDRLLEONCR 394  
 DB 336 NPLQKMEASA-HKQSLDTPDTPATLYAVVENVPPLRMKEFVRRLGLSDHEIDRLLEONCR 394  
 QY 411 HLEAQSMLAAMRRRTTPREATTLELGRVLRMDMLGCLLENIEBALGGAARLASERPLL 470  
 DB 411 HLEAQSMLAAMRRRTTPREATTLELGRVLRMDMLGCLLENIEBALGGAARLASERPLL 470  
 QY 395 CLREAOYSMLATWRRRTTPREATTLELGRVLRMDMLGCLLENIEBALGGAARLASERPLL 454  
 DB 395 CLREAOYSMLATWRRRTTPREATTLELGRVLRMDMLGCLLENIEBALGGAARLASERPLL 454

## RESULT 5

AAR10986  
 ID AAR10986 standard; Protein; 455 AA.

XX AAR10986;

XX 25-MAR-2003 (updated)  
 DT 13-MAY-1991 (first entry)

XX 30KD TNF inhibitor precursor.

XX Tumour necrosis factor; inhibitor.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Cleavage-site 40..41  
 FT note="cleavage gives active protein"

XX AU9058976-A.

XX 24-JAN-1991.

XX 16-JUL-1990; 90AU-0058976.

XX 07-FEB-1990; 90US-0479661.

XX 18-JUL-1989; 89US-0381080.

XX 11-DEC-1989; 89US-0450329.

XX (SYND) SYNERGEN INC.

XX WPI; 1991-073847/11.

XX N-PSDB; AAQ10883.

XX Tumour necrosis factor inhibitor - for suppression of TNF-alpha

XX and -beta, useful as therapeutic agent.

XX Disclosure: Fig 21; 142p; English.

XX The sequence comprises the entire 30 kD TNF inhibitor. The clone

XX from which the sequence was deduced was isolated from a cDNA

XX library prep'd. from RNA form U937 cells treated with PMA/PHA.

CC of TNF inhibitor for use in the treatment of inflammatory and  
 CC degenerative diseases. The active protein is claimed (Claim 8).  
 CC See also AAR10984 and AAR1001.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX

SO Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 12; Length 455;  
 Best Local Similarity 62.9%; Pred. No. 1.4e-95;  
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLTPVPGDLLPLVLPALLADVPYGVGVPHRPEDEKESPPCQKYNPNOSTICT 60  
 DB 1 MGLTPVPGDLLPLVLPALLADVPYGVGVPHRPEDEKESPPCQKYNPNOSTICT 60  
 QY 61 KCHKGTLYNDGPGRDPTDCRCVACPTTALLENHRLCLSCRCRDEMFOVEISPCVVD 120  
 DB 61 KCHKGTLYNDGPGRDPTDCRCVACPTTALLENHRLCLSCRCRDEMFOVEISPCVVD 120  
 QY 121 RDTVCGCRKQRYREYWGSTGFRCLNCSLCPNGTVNI PCOERODTICHCHMGFFLKAKCI 180  
 DB 121 RDTVCGCRKQRYREYWGSTGFRCLNCSLCPNGTVNI PCOERODTICHCHMGFFLKAKCI 180  
 QY 181 SCHDCRKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLASFAVYLACRYQRWK 239  
 DB 181 SCHDCRKN-ECEKLCPTPSTGKDSODPGTTVLLPLVIFGLCLASFAVYLACRYQRWK 239  
 QY 240 PKYXIIICGOSTLVKEGPE-----LVVAPGPNP-----TTTICFSTSPSSSPVSIIPPYI 290  
 DB 240 PKYXIIICGOSTLVKEGPE-----LVVAPGPNP-----TTTICFSTSPSSSPVSIIPPYI 290  
 QY 291 SCDSNFGAVASPSSETAPRHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350  
 DB 291 SCDSNFGAVASPSSETAPRHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350  
 QY 301 PGDCPNF---AARREVAPPYOGADPIL-----ATML-----ASDP1P 335  
 DB 301 PGDCPNF---AARREVAPPYOGADPIL-----ATML-----ASDP1P 335  
 QY 351 TPVQKMEASAPSPDOLADADPATLYAVVDGVPSPRWKELVRRLGLSEHEIERLEENGR 410  
 DB 351 TPVQKMEASAPSPDOLADADPATLYAVVDGVPSPRWKELVRRLGLSEHEIERLEENGR 410  
 QY 336 NPLQKMEASA-HKQSLDTPDTPATLYAVVENVPPLRMKEFVRRLGLSDHEIDRLLEONCR 394  
 DB 336 NPLQKMEASA-HKQSLDTPDTPATLYAVVENVPPLRMKEFVRRLGLSDHEIDRLLEONCR 394  
 QY 411 HLEAQSMLAAMRRRTTPREATTLELGRVLRMDMLGCLLENIEBALGGAARLASERPLL 470  
 DB 411 HLEAQSMLAAMRRRTTPREATTLELGRVLRMDMLGCLLENIEBALGGAARLASERPLL 470  
 QY 395 CLREAOYSMLATWRRRTTPREATTLELGRVLRMDMLGCLLENIEBALGGAARLASERPLL 454  
 DB 395 CLREAOYSMLATWRRRTTPREATTLELGRVLRMDMLGCLLENIEBALGGAARLASERPLL 454

## RESULT 6

AAR42059  
 ID AAR42059 standard; Protein; 455 AA.

XX AAR42059;

XX 25-MAR-2003 (updated)

DT 29-APR-1994 (first entry)

XX Lambda derived TNF-R.

XX Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;

XX IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;

XX rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;

XX pulmonary fibrosis; sickle cell; allograft; xenograft; rejection;

XX graft versus host disease; sepsis; inflammation; allergy;

XX autoimmune dysfunction.

XX Homo sapiens.

XX Lambda-gt10-7ctnfbp.

XX Key Location/Qualifiers

XX Peptide 1..40  
 FT /note="Signal peptide"

XX Protein 41..455  
 FT /note="Mature hTNF-R"

XX W09319777-A1.



PD 14-OCT-1993.  
 XX PF 26-MAR-1993; 93WO-US02938.  
 XX PR 30-MAR-1992; 92US-0860710.  
 XX PA (IMMV ) IMMUNEX CORP.  
 XX PI Smith CA;  
 XX DR WPI; 1993-336592/42.  
 XX N-PSDB; AAQ49932.  
 PT New fusion protein tumour necrosis factor and human interleukin-1  
 PT receptor - useful in therapy, diagnosis and assays of e.g.  
 PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.  
 PS Disclosure; Page 57-59; 85pp; English.  
 XX  
 CC The sequences given in AAR42058-59 represent human tumour necrosis  
 CC factor receptor (TNF-R) and the sequences in AAR42060-61 represent  
 CC human interleukin-1 receptor (IL-1R). These sequences were used in  
 CC the production of a fusion protein which conformed to one of the  
 CC formulae:  
 CC TNF-R-linker-TNF-R-linker-IL-1R  
 CC IL-1R-linker-TNF-R-linker-TNF-R or  
 CC TNF-R-linker-TNF-R  
 CC The linker may comprise 5-100 amino acids selected from Gly, Asp,  
 CC Ser, Thr and Ala. These linkers separate the individual moieties  
 CC by such a distance that each component of the fusion protein is  
 CC capable of folding into the secondary or tertiary structure required  
 CC for its biological activity. These fusion proteins may be used in  
 CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,  
 CC particularly in conditions in which both TNF and IL-1 play a causative  
 CC role. They may be used to treat cachexia, rheumatoid arthritis,  
 CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,  
 CC cerebral malaria, allograft and xenograft rejection in graft versus  
 CC host disease, sepsis, septic shock, inflammation, allergies and  
 CC autoimmune dysfunctions.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SO Sequence 455 AA;  
 Query Match 58.3%; Score 1517; DB 14; Length 455;  
 Best Local Similarity 62.9%; Pred. NO.1.4e-95;  
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

DB 336 NPLQKMEDSA-HKRFQSLDTPDPAITYAVENVDPPLRNKEFVRRLGSLDSHEIDRLLEONGR 394  
 OY 411 HLRFAQYSMLAARRRTPREATLELLGRVLRDMDLGCTLENIEAALGAARLASEPRLL 470  
 DB 395 CLRBAQYSMLATRRRRTPREATLELLGRVLRDMDLGCTLENIEAALGAARLASEPRLL 454  
 RESULT 7  
 ID AAR75084  
 AAR75084 standard; Protein; 455 AA.  
 AC AAR75084;  
 DT 19-JAN-1996 (first entry)  
 XX p55 TNF-R.  
 XX p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;  
 KW epidermal growth factor receptor; EGF-R; protease; inhibitor;  
 KW phorbol myristate acetate; PMA.  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Peptide  
 FT /location/Qualifiers  
 FT /note= "N terminus of soluble p55 TNF-R"  
 FT /note= 54..56  
 FT Modified-site  
 FT /note= "glycosylation site"  
 FT /note= 145..147  
 FT Modified-site  
 FT /note= "glycosylation site"  
 FT /note= 161..163  
 FT Peptide  
 FT /note= "glycosylation site"  
 FT /note= 193..210  
 FT Peptide  
 FT /note= "peptide used in creation of chimeras"  
 FT /note= 198..210  
 FT Region  
 FT /note= "spacer region"  
 FT Misc-difference  
 FT /note= "major C terminus for soluble p55 TNF-R"  
 FT /note= 201  
 FT Misc-difference  
 FT /note= "essential for shedding reaction"  
 FT /note= 202  
 FT Misc-difference  
 FT /note= "minor C terminus for soluble p55 TNF-R"  
 FT /note= 203  
 FT Region  
 FT /note= "transmembrane region"  
 FT /note= 212..234  
 PN AU9475742-A.  
 PD 04-MAY-1995.  
 XX 11-OCT-1994; 94AU-0075742;  
 PF 12-OCT-1993; 93IL-0107268.  
 PR (YEDA ) YEDA RES & DEV CO LTD.  
 PA  
 XX  
 PI Backin M, Brakebusch C, Varfolomeev E, Wallach D;  
 DR WPI; 1995-194342/26.  
 XX N-PSDB; AAQ90513.  
 PT New protease capable of cleaving soluble tumour necrosis factor  
 PT (TNF) receptor - from cell-bound TNF- receptor, useful for  
 PT antagonising deleterious effects of TNF.  
 XX  
 PS Disclosure; Fig 1; 40pp; English.  
 XX This sequence represents human p55 tumour necrosis factor (TNF-R).  
 CC Expression of this receptor is regulated by shedding of the  
 CC extracellular receptor fragment. The p55 TNF-R can be shed in response  
 CC to different inducing agents, e.g. phorbol myristate acetate (PMA),  
 CC depending on cell type. The only region of the receptor whose structure  
 CC affects the shedding response is the spacer region (see AAR75012) in the  
 CC extracellular domain. This region is located close to a site of cleavage

of the molecule, and links the Cys rich module to the transmembrane domain. The spacer region of the encoded protein was used to create the chimera between human p55 TNF-R and murine epidermal growth factor receptor (EGF-R) that are represented by AAR75007-11. This spacer region was subjected to deletion mutations (AAR75013-25) and substitutions (AAR75026-47). Of the spacer region, the most important residues are Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most important of these. The shedding of the receptor is independent of the side chain identity of these residues, with the exception of a limited dependence on the identity of Val 173. Mutations which alter the conformation of the protein adversely effect the shedding process. The mutations shown in AAR75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TNF-R from the cell bound TNF-R. Fragments of these inhibitors can be seen in AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease inhibitors can be used for enhancing TNF function.

Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 16; Length 455;

Best Local Similarity 62.9%; Pred. No. 1,4e-95;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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OY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGKYNHPONSTICT 60
DB 1 MGLSTVPDLLPLVLLELVGLVPSGVIGLVPHLGREKRDSDVCPGKXIHPPONNSICT 60
OY 61 KCHKGTLYLNDPCPGRDTCRCVCAFGTYTALLENHRLCLSCSRCDENMFQVEISPCVVD 120
DB 61 KCHKGTLYLNDPCPGRDTCRCESGSGFTASENHLRHCLSCSKCKEMGQVEISSCTVD 120
OY 121 RDTVCGCRKNQRYRWGEGTGRCLNCSLCPNGTVINPCOERODTICHHMGFFLKAKCI 180
DB 121 RDTVCGCRKNQRYRWGSENLFCQCFNCSLCNLTGTHLSCEKONTVCTCHAGFFLENECV 180
OY 181 SCHDCKNK-ECEKLCPTRPSTGKSDPGTTLVPLVIFGLCLASPASVVLACYGRWK 239
DB 181 SCNNCKSKLECKTCLCPQLENVKGTEDSGTTLVPLVIFGGLCLSLFLTGIMRYGRWK 240
OY 240 PLVYSIIIGOSTLVNKGEP-----LVVAPGPNP-----TTTICPSSSSPVGIPPI 290
DB 241 SKLVISIVCKSTPEKEGLEGTTTYPRLAPNPFSSPPGCTPLGSPVSSFTSSSTYT 300
OY 291 SCDSNFCGAVASPSSETAPRLKAGPILEGPPASTHLCTPGPASTHLCTPGPASTHL 350
DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPPIP 335
OY 351 TPVQKWEASAPAPQADADPATIYAVYDGVPPSKWEKLVRLGLSEHIEIRLENGR 410
DB 336 NPLQKWEESA-HKPSQLDTDDPATIYAVVENVPPLRKKEFVRLGISDHEIDRLQLONGR 394
OY 411 HLREAQVSMALAMRRRTPRREATLELGLVRLDMDLGLCLNIEEALGGAARLASERPL 470
DB 395 CLREAQVSMALAMRRRTPRREATLELGLVRLDMDLGLCLNIEEALGGAARLASERPL 454

```

RESULT 8

AAV30934

ID AAV30934 standard; Protein; 455 AA.

XX AAV30934;

DT 20-MAR-2003 (updated)

XX 18-OCT-1999 (first entry)

DE Human tumour necrosis factor binding protein.

KM Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;  
 KM anti-inflammatory; antimalarial; treatment; septic shock; inflammation;  
 KM autoimmune glomerulonephritis; cerebral malaria; immune response;  
 KM antagonist; diagnosis.

O5 Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..29  
 FT /label= signal\_peptide  
 FT Protein 30..455  
 FT Modified-site 34  
 FT /note= "hypothetical glycosylation site"  
 FT Modified-site 125  
 FT /note= "hypothetical glycosylation site"  
 FT Modified-site 131  
 FT /note= "hypothetical glycosylation site"  
 FT Region 212..230  
 FT /note= "transmembrane region"  
 FT Modified-site 250  
 FT /note= "hypothetical glycosylation site"

PN EP939121-A2.

PD 01-SEP-1999.

PP 31-AUG-1990; 99EP-0100703.

PR 12-SEP-1989; 89CH-0003319.

PR 08-MAR-1990; 90CH-0000746.

PR 20-APR-1990; 90CH-0001347.

PR 31-AUG-1990; 90EP-0116707.

PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.

PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;

PI Schlaeger E;

DR MPI: 1999-480840/41.

DR N-PSDB; AA209170.

XX New insoluble proteins, and fragments, that bind to tumor necrosis

PT factor, used to treat e.g. septic shock or cerebral malaria

PS Claim 4a; Fig 1; 25pp; German.

XX This invention describes novel homogeneous insoluble proteins (I),

CC their (in)soluble fragments (Ia) and their salts that can bind tumour

CC necrosis factor (TNF). The products of the invention have

CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)

CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune

CC glomerulonephritis, cerebral malaria, immune responses and inflammation),

CC (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for

CC diagnostic determination of TNF in body fluids. Antibodies raised against

CC (I) are used for affinity purification of (I). This sequence represents

CC a tumour necrosis factor binding protein described in the method of

CC the invention.

CC (Updated on 20-MAR-2003 to correct PR field.)

CC (Updated on 20-MAR-2003 to correct PR field.)

SO Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 20; Length 455;

Best Local Similarity 62.9%; Pred. No. 1,4e-95;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```

OY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGKYNHPONSTICT 60
DB 1 MGLSTVPDLLPLVLLELVGLVPSGVIGLVPHLGREKRDSDVCPGKXIHPPONNSICT 60
OY 61 KCHKGTLYLNDPCPGRDTCRCVCAFGTYTALLENHRLCLSCSRCDENMFQVEISPCVVD 120
DB 61 KCHKGTLYLNDPCPGRDTCRCESGSGFTASENHLRHCLSCSKCKEMGQVEISSCTVD 120
OY 121 RDTVCGCRKNQRYRWGEGTGRCLNCSLCPNGTVINPCOERODTICHHMGFFLKAKCI 180
DB 121 RDTVCGCRKNQRYRWGSENLFCQCFNCSLCNLTGTHLSCEKONTVCTCHAGFFLENECV 180
OY 181 SCHDCKNK-ECEKLCPTRPSTGKSDPGTTLVPLVIFGLCLASPASVVLACYGRWK 239

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Db      181 SCNCKSLSECTKLCLEPIENVKGTEDSGTTLPLVIFGLCLSLFLIGLMRYQRMK 240
Qy      240 PKLYSIICGOSTLYKEGEPE-----LLVPAAGFNP-----TTTICFSSTPSSSPVSIPIYI 290
Db      241 SKLYSIIVCGKSTPEKEGELBETTTKPLAPNPSFSPFTGLGSPVPSSTFTSSSTYT 300
Qy      291 SCDSNPGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTGPPASTHLCTC 350
Db      301 PGDCPNF---AAPREVAPPYOGADPIL-----ATLA-----ASDPIIP 335
Qy      351 TPVCKMEASAPASPDQADADPATLYAVVGVPSRMELEVRRLGSLSEHEIERLEENGR 410
Db      336 NPLQKMEBSA-HKQOSLDTDDPATILYAVENVPLRWKEFVRRLGLSDHEIDRIELQNGR 394
Qy      411 HLEAQSMLAAWRRTTREPRTATTELLGRVLRDMDLGLCLENIEBALGGAARLASERPLL 470
Db      395 CLREAQYSMLATWRRRTTREPRTATTELLGRVLRDMDLGLCLENIEBALGGAARLASERPLL 454

```

## RESULT 9

AAB36266 ID AAB36266 standard; Protein; 455 AA.

XX AC AAB36266;

DT 20-FEB-2001 (first entry)

DE Human tumour necrosis factor receptor 1.

KM Human: death domain containing receptor; DR3-VI; cancer;  
 KW autoimmune disorder; inflammation; cardiovascular disorder; infection;  
 KM neurodegenerative disease; angiogenesis.

OS Homo sapiens.

XX MO200064465-A1.

PN 02-NOV-2000.

PF 21-APR-2000; 2000WO-US10741.

XX 22-APR-1999; 99US-0130488.

PR 28-MAY-1999; 99US-0136741.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

PA (YUGG/) YU G.

PA (NIJJ/) NI J.

PA (GENT/) GENTZ R L.

PA (DILL/) DILLON P J.

PA (DIXI/) DIXIT V M.

PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;

DR WPI; 2000-687263/67.

PT Treating graft-versus-host disease, cancer, immunodeficiency or an  
 PT autoimmune disease comprising administering an antibody to Death Domain  
 PT Containing Receptor proteins and a second therapeutic agent -

XX Disclosure; Fig 3; 273pp; English.

XX The present invention provides the protein and coding sequences for two  
 CC death domain containing receptors, designated DR3 and DR3-VI. These  
 CC receptors are involved in apoptosis, and the sequences given can be used  
 CC in the treatment of cancers, infections, cardiovascular disorders such as  
 CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms  
 CC and congenital heart defects, neurodegenerative diseases including  
 CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple  
 CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,  
 CC and to promote angiogenesis and wound healing.

50 Sequence 455 AA:

Query Match 58.3%; Score 1517; DB 21; Length 455;  
 Best Local Similarity 62.9%; Pred. No. 1.4e-95;  
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```

Qy      1 MGLPTVRELPLPLPALADVPAGVQGLVPHFGDLKEKESPPQCKKYNHPONSTICT 60
Db      1 MGLSTVDPDLLPLLELLELVGIVPSGVIGLVPHLGDREKRSVCPQCKYIHPONNSICT 60
Qy      61 KCHGKTYLVNDPCPGRBDTCRCVAPGTATLLENHLRRCSCSRCPREMPVEIISPCYVD 120
Db      61 KCHGKTYLVNDPCPGQDTCRCBESGFTASNNHLRHCSCSKCKRMGQVEIISCTVD 120
Qy      121 RDTVCGKKNQRYREYWGSETGFCINCSLCPNGTVNIPCOERODTICCHMGFPFLKAKCI 180
Db      121 RDTVCGKKNQRYRYWENLFCFCNCSLCLNGTVHLSQGBQKNVTCTCHAGFLRENECV 180
Qy      181 SCHDCRKN-EGCKLCPTRPSTGKDSQDPGTVLLPLVIYVGLCLASFPASVTLACRYQRMK 239
Db      181 SCNCKSLSECTKLCLEPIENVKGTEDSGTTLPLVIFGLCLSLFLIGLMRYQRMK 240
Qy      240 PKLYSIICGOSTLYKEGEPE-----LLVPAAGFNP-----TTTICFSSTPSSSPVSIPIYI 290
Db      241 SKLYSIIVCGKSTPEKEGELBETTTKPLAPNPSFSPFTGLGSPVPSSTFTSSSTYT 300
Qy      291 SCDSNPGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTGPPASTHLCTC 350
Db      301 PGDCPNF---AAPREVAPPYOGADPIL-----ATLA-----ASDPIIP 335
Qy      351 TPVCKMEASAPASPDQADADPATLYAVVGVPSRMELEVRRLGSLSEHEIERLEENGR 410
Db      336 NPLQKMEBSA-HKQOSLDTDDPATILYAVENVPLRWKEFVRRLGLSDHEIDRIELQNGR 394
Qy      411 HLEAQSMLAAWRRTTREPRTATTELLGRVLRDMDLGLCLENIEBALGGAARLASERPLL 470
Db      395 CLREAQYSMLATWRRRTTREPRTATTELLGRVLRDMDLGLCLENIEBALGGAARLASERPLL 454

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## RESULT 10

AAB37800 ID AAB37800 standard; Protein; 455 AA.

XX AAB37800;

DT 23-FEB-2001 (first entry)

DE Human tumour necrosis factor p55 receptor.

KM Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;  
 KW p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;  
 KW immunosuppressive; immunomodulator; cardiac; cystostatic; cachexia;  
 KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;  
 KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;  
 KW chronic myelogenous leukaemia; inflammatory bowel disease.

OS Homo sapiens.

XX MO200064479-A1.

PN 02-NOV-2000.

PF 26-APR-2000; 2000WO-US11700.

XX 27-APR-1999; 99US-0301274.

XX (ANT1-) ANTIBODY SYSTEMS INC.

PA Fredeking TM, Ignatjev GM;

PI WPI; 2000-679646/66.

PT Novel compositions comprising tetracycline or tetracycline-like

PT compounds for the treatment and/or prevention of acute inflammatory  
PT responses and diseases, e.g. septic shock and immune complex-induced  
PT colitis -

XX Disclosure; Page 167-169; 183pp; English.

XX The present sequence is given in a specification relating to novel  
XX compositions and methods containing tetracycline or tetracycline-like  
XX compounds for treating and/or preventing acute inflammatory responses and  
XX diseases. Such diseases include acute inflammatory conditions associated  
XX with viral haemorrhagic diseases (including diseases caused by  
XX Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),  
XX parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune  
XX disorders, acute cardiovascular events, chronic myelogenous leukaemia and  
XX transplanted bone marrow-induced graft-versus-host disease, septic shock,  
XX immune complex-induced colitis, cerebrospinal fluid inflammation,  
XX multiple sclerosis, inflammatory responses associated with trauma,  
XX systemic inflammatory response syndrome (SIRS), adult respiratory  
XX distress syndrome (ARDS), acute liver failure, inflammatory bowel disease  
XX and Crohn's disease.

XX Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 21; Length 455;  
Best Local Similarity 62.9%; Pred. No. 1.4e-95;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```

QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPDLEKRESPCQGRKYNHPNSTICT 60
DB 1 MGLSTVPDLLPLVLLELVGIGLVPHLDREKRSQVCPQGRKYNHPNSTICT 60
QY 61 KCHKGTLYNDPCPGRDTCRCVCAFGTYTALLENHRLRCLSCSRGRDMPFVEISPCVVD 120
DB 61 KCHKGTLYNDPCPGRDTCRCVCAFGTYTALLENHRLRCLSCSRGRDMPFVEISPCVVD 120
QY 121 RDTVCGCRKNQYREYWGTFRCNLSLCPNGTVNIPCOERODTICHGMGFPLGAKCI 180
DB 121 RDTVCGCRKNQYREYWGTFRCNLSLCPNGTVNIPCOERODTICHGMGFPLGAKCI 180
QY 121 RDTVCGCRKNQYREYWGTFRCNLSLCPNGTVNIPCOERODTICHGMGFPLGAKCI 180
DB 121 RDTVCGCRKNQYREYWGTFRCNLSLCPNGTVNIPCOERODTICHGMGFPLGAKCI 180
QY 181 SCHDCKNK-EECKLCPTPSTGKSDQDPTVLLPLVIFGLCLASFPASVVLACRYQRMK 239
DB 181 SCHDCKNK-EECKLCPTPSTGKSDQDPTVLLPLVIFGLCLASFPASVVLACRYQRMK 239
QY 181 SCNNCKSLKCTKCLPOLIENVKGTEDSGTTLPLVIFGLCLASFPASVVLACRYQRMK 240
DB 181 SCNNCKSLKCTKCLPOLIENVKGTEDSGTTLPLVIFGLCLASFPASVVLACRYQRMK 240
QY 240 PKLYSIICGOSTLVKEGEP-----LVVPAGFNP-----TTTICFSSPTSSSPVSIPIYI 290
DB 240 PKLYSIICGOSTLVKEGEP-----LVVPAGFNP-----TTTICFSSPTSSSPVSIPIYI 290
QY 241 SKLYSIIVCGKSTPEKEGLEGTITTKPLAPNPSFPTPGFTPLGSPVPSSTFTSSSTYT 300
DB 241 SKLYSIIVCGKSTPEKEGLEGTITTKPLAPNPSFPTPGFTPLGSPVPSSTFTSSSTYT 300
QY 291 SCDSNPGAVASPSSETAPPHLKAGPILGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
DB 291 SCDSNPGAVASPSSETAPPHLKAGPILGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
QY 301 PGDCPNF---AAPREVAPPYQADPIL-----ATAL-----ASDPIP 335
DB 301 PGDCPNF---AAPREVAPPYQADPIL-----ATAL-----ASDPIP 335
QY 351 TPVQKMEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRRLGSLSEHIERLENGR 410
DB 351 TPVQKMEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRRLGSLSEHIERLENGR 410
QY 336 NPLQWEDSA-HKPSLDLTDPATLYAVVENPPLRWKEFVRLGSLSEHIERLENGR 394
DB 336 NPLQWEDSA-HKPSLDLTDPATLYAVVENPPLRWKEFVRLGSLSEHIERLENGR 394
QY 411 HLREAOYSLAAMRRTPRBEATLELGRVLRDMDLGLCLENIEEALGGAARLASEPPL 470
DB 411 HLREAOYSLAAMRRTPRBEATLELGRVLRDMDLGLCLENIEEALGGAARLASEPPL 470
QY 355 CLREAOYSLAAMRRTPRBEATLELGRVLRDMDLGLCLENIEEALGGAARLASEPPL 454
DB 355 CLREAOYSLAAMRRTPRBEATLELGRVLRDMDLGLCLENIEEALGGAARLASEPPL 454

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RESULT 11

AAB26984 ID AAB26984 standard; Protein; 455 AA.

XX AAB26984;

XX 02-FEB-2001 (first entry)

XX Human TNFR 1.

XX Human, TNFR 1, tumour necrosis factor; TR9 receptor; immunosuppressive;  
XX antiinflammatory; cardiant; antiaesthetic; antidiabetic; antiallergic;  
XX antiaesthetic; antineumatic; anti-HIV; anticonvulsant; cytostatic;

KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;  
KW common variable immunodeficiency; X-linked agammaglobulinemia;  
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;  
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;  
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;  
KW cardiovascular disease; neurological disease; protein coordinate data.

XX Homo sapiens.

XX WO200056862-A1.

XX 28-SEP-2000.

XX 16-MAR-2000; 2000WO-US06831.

XX 24-MAR-1999; .99US-0126019.

XX 14-MAY-1999; 99US-0134220.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Geniz RL, Yu G, Fan P;

XX WPI; 2000-594575/56.

PT Nucleic acid molecule encoding a human tumor necrosis factor receptor,  
PT known as TR9, useful for treating, preventing and diagnosing severe  
PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy  
PT and cancer -

XX Disclosure; Fig 2; 220pp; English.

XX The present sequence is TNFR 1, a member of the tumour necrosis factor  
XX receptor family. A novel human tumour necrosis factor receptor,  
XX designated TR9, has been isolated. The TR9 receptor is also known as  
XX Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or  
XX agonists are useful for treating, preventing or diagnosing common  
XX variable immunodeficiency, X-linked agammaglobulinemia, severe combined  
XX immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such  
XX as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis,  
XX diabetes mellitus and asthma), HIV infection, epilepsy, cancer,  
XX cardiovascular diseases and other neurological diseases.

XX Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 21; Length 455;  
Best Local Similarity 62.9%; Pred. No. 1.4e-95;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

```

QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPDLEKRESPCQGRKYNHPNSTICT 60
DB 1 MGLSTVPDLLPLVLLELVGIGLVPHLDREKRSQVCPQGRKYNHPNSTICT 60
QY 61 KCHKGTLYNDPCPGRDTCRCVCAFGTYTALLENHRLRCLSCSRGRDMPFVEISPCVVD 120
DB 61 KCHKGTLYNDPCPGRDTCRCVCAFGTYTALLENHRLRCLSCSRGRDMPFVEISPCVVD 120
QY 121 RDTVCGCRKNQYREYWGTFRCNLSLCPNGTVNIPCOERODTICHGMGFPLGAKCI 180
DB 121 RDTVCGCRKNQYREYWGTFRCNLSLCPNGTVNIPCOERODTICHGMGFPLGAKCI 180
QY 121 RDTVCGCRKNQYREYWGTFRCNLSLCPNGTVNIPCOERODTICHGMGFPLGAKCI 180
DB 121 RDTVCGCRKNQYREYWGTFRCNLSLCPNGTVNIPCOERODTICHGMGFPLGAKCI 180
QY 181 SCHDCKNK-EECKLCPTPSTGKSDQDPTVLLPLVIFGLCLASFPASVVLACRYQRMK 239
DB 181 SCHDCKNK-EECKLCPTPSTGKSDQDPTVLLPLVIFGLCLASFPASVVLACRYQRMK 239
QY 181 SCNNCKSLKCTKCLPOLIENVKGTEDSGTTLPLVIFGLCLASFPASVVLACRYQRMK 240
DB 181 SCNNCKSLKCTKCLPOLIENVKGTEDSGTTLPLVIFGLCLASFPASVVLACRYQRMK 240
QY 240 PKLYSIICGOSTLVKEGEP-----LVVPAGFNP-----TTTICFSSPTSSSPVSIPIYI 290
DB 240 PKLYSIICGOSTLVKEGEP-----LVVPAGFNP-----TTTICFSSPTSSSPVSIPIYI 290
QY 241 SKLYSIIVCGKSTPEKEGLEGTITTKPLAPNPSFPTPGFTPLGSPVPSSTFTSSSTYT 300
DB 241 SKLYSIIVCGKSTPEKEGLEGTITTKPLAPNPSFPTPGFTPLGSPVPSSTFTSSSTYT 300
QY 291 SCDSNPGAVASPSSETAPPHLKAGPILGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
DB 291 SCDSNPGAVASPSSETAPPHLKAGPILGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
QY 301 PGDCPNF---AAPREVAPPYQADPIL-----ATAL-----ASDPIP 335
DB 301 PGDCPNF---AAPREVAPPYQADPIL-----ATAL-----ASDPIP 335
QY 351 TPVQKMEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRRLGSLSEHIERLENGR 410
DB 351 TPVQKMEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRRLGSLSEHIERLENGR 410

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Dd		336 NPLQKWEESA-HKPGSLDTDDPATIYAVAVENPPLRMKEFVRLTGISDHEIDBLELONGR	394
Oy		411 HLEBAQVYSMLAAMRRRTTPREKATLILGCVLRDMDLGLCTLENIEEALGGARLASPRLL	470
Dd		395 CLREAOYSMLATWRRTTRREATLEHLIGVRMDMGLGLEDEIEEALCGPALPPASILL	454
		RESULT 12	
	AAB23446		
ID	AAB23446	standard; Protein; 455 AA.	
XX	AAC		
XX	AAB23446;		
DT	12-JAN-2001	(first entry)	
DE	Human tumour necrosis factor receptor 1 protein.		
XX	TNFR1; tumour necrosis factor receptor; polymorphism; human;		
KM	tumour; cancer; apoptosis; bacterial infection.		
OS	Homo sapiens.		
XX	WO2000050436-A1.		
PN			
PD	31-AUG-2000.		
XX			
PF	23-FEB-2000; 2000WO-US04606.		
PR	23-FEB-1999; 99US-0121314.		
XX			
PA	(GENA-) GENAISANCE PHARM INC.		
PA	(NAND/) NANDABALAN K.		
PA	(SCHU/) SCHULZ V P.		
PA	(STEP/) STEPHENS J C.		
PA	(CHEW/) CHEW A.		
XX			
PI	Nandabalan K, Schulz VP, Stephens JC, Chew A;		
DR	WPI; 2000-543909/49.		
XX	N-PSDB; AAA95105.		
PT	Polymucleotides comprising polymorphic variants of a reference sequence		
PT	for tumour necrosis factor receptor 1 (TNFR1), useful for studying the		
PT	biological function of TNFR1 and identifying drugs targeting the		
XX	protein for treating disorders -		
PS			
XX	Claim 10; Fig 5; 79pp; English.		
CC	The present invention relates to polymorphic variants of the tumour		
CC	necrosis factor receptor 1 (TNFR1) gene. The present sequence is		
CC	the TNFR1 protein. The sequence of the whole gene is given in AAA95102,		
CC	AAA95103 and AAA95104. The polymorphisms were identified by amplifying		
CC	and sequencing regions of the gene. Twelve polymorphic loci		
CC	were discovered. Of these twelve polymorphisms, four can cause a		
CC	change in the TNFR1 protein. The TNFR1 polymorphisms may be useful		
CC	for studying the biological function of TNFR1 as well as for		
CC	identifying drugs targeting the protein for treatment of disorders		
CC	related to its abnormal expression or function such as tumours,		
CC	apoptosis related disorders and bacterial infection.		
XX			
SO	Sequence 455 AA:		
	Query Match 58.3%; Score 1517; DB 21; Length 455;		
	Best Local Similarity 62.9%; Pred. No. 1.4e-95;		
	Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7		
Oy		1 MGLPVIVPGCLLPVLVPALLADVYPAGVGGLVHPHGDLEKRBSGPCGCKNHNPNSITICT	60
Dd		1 MGLSTVPDLLPLVLYLELVGVISGVIGLVPHLGIRERKRDSDVCPOGKYIHPPNNISICT	60
Oy		61 KCHKTYLYNDPCRGGRDTCGVCAAGVTYTALENHRRLCSGRCGDEMDFOVISPCVD	120

Db	6	KCHKGTYLVNDOPRGQDPTDCRECESSGFASENHLHCLSCSKCREMGOVEISSCTVD	120
Qy	121	RDTVCCGRKNQYREYWGTEGFRCLNCLSCIPNGTVNIPCOERODTICHGNGFLKAKCI	180
Db	121	RDVCCGRKNQYRHWSENILFCFCFNCSCILNGTHTLSCOEKONTVCTCHAGFLRENECV	180
Qy	181	SCDCKCNK--ECKKLCPTBPSYKGSODPGTTLVLLPLVYVGLCLASPAVVLACRYORWK	239
Db	181	SCSNCKKSLCKTKLCPQIENVKGTEDSGTIVLLPLVIFELCLSLPFIGLMYRORWK	240
Qy	240	PKLYSIICQSTLVKEGEPE-----LVPARGFNP-----TTTICFSSTPSSSPVSIPIYI	290
Db	241	SKLYSIIVCKSKYIPKKEGELGETTTPKLANPNSFPTGFPPTLGFSVPSTFTSSSTYT	300
Qy	291	SCDRSNFGAVASPSSETPAPHLKAGPIIPGPPASTHLCTGPPASTHLCTPPGPASTHLC	350
Db	301	PGCGCPNF--AAPREVAAPYCGADPIL-----ATPL-----ASDPIIP	335
Qy	351	TPYQKKEASAPAPQGLADAPATLYAVVDGVPSPMKELVRYRIGLSEHEIRLENGR	410
Db	336	NPLQKKEDSA-HKPSLDTDDPATLYAVENVPLRMKEFVRRLGSLDHEIDRLQLNGR	394
Qy	411	HUREAOYSMLAARRRTPREATYLELGRVLRDMDLGSCLNTIEBALGGAARLASBPRLL	470
Db	395	CUREAOYSMLATMRRTTRRENTIELGRVLRDMDLGSCLNIEBALCGRALPPAPSL	454
RESULT 13			
AA	01336	AAAB01336 standard; Protein; 455 AA.	
AC	AAAB01336;		
XX	25-SBP-2000 (first entry)		
XX	TNF-R1 death receptor.		
XX	UL144; death receptor; apoptosis; programmed cell death; FAS;		
XX	KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;		
XX	human.		
XX	Homo sapiens.		
XX	NC0200034335-A2.		
XX	15-JUN-2000.		
XX	03-DEC-1999; 99MO-US26035.		
XX	04-DEC-1998; 98US-0205018.		
XX	(SCHE ) SCHERING CORP.		
XX	Leong C, Phillips JH;		
XX	MP1; 2000-423383/36.		
XX	Purified or recombinant polypeptide for modulating apoptosis comprises		
XX	a sequence which binds to an antibody specific for UL144 or its		
XX	fragments		
XX	Disclosure, Page 65-67; 76pp; English.		
XX	A pure or recombinant polypeptide which binds to a polyclonal antibody		
XX	specific for the mature UL144 is useful for screening molecules which		
XX	block induction of apoptosis or interfere with antiapoptotic activity.		
XX	The polypeptide is also useful for modulating apoptosis and useful in		
XX	treatment of conditions associated with abnormal physiology or		
XX	development, such as cancer or degenerative conditions and for		
XX	regulation of viral infection and replication. At least five		
XX	different death receptors are known, which include the CD95		
XX	(Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated		
XX	protein (TRAMP), death receptor-6 (DR-6), and TNF-related		

CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.  
 XX Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 21; Length 455;  
 Best Local Similarity 62.9%; Pred. No. 1.4e-95;  
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

OY 1 MGLPTVPGLLPLVLPALLADVPAGVGVLPHPDLEKRESPPQCKYHNPNSTICT 60  
 DB 1 MGLSTVPDLPLPLVLLELVGIVPSGVGLVPHLDREKRSVCPQKGIHPQNNSTICT 60  
 OY 61 KCHKGTVLYNDPCPGPGRDTCRCVCAPGTYTALENHRLRCLSCSRGDEMFWVEISPCVVD 120  
 DB 61 KCHKGTVLYNDPCPGPGRDTCRCVCAPGTYTALENHRLRCLSCSRGDEMFWVEISPCVVD 120  
 OY 121 RDTVCGCRKNQRYRYWSEGTGFRCLNCSLCPNGTINI PCOERODTICHGMGFLLGAKCI 180  
 DB 121 RDTVCGCRKNQRYRYWSEGTGFRCLNCSLCPNGTINI PCOERODTICHGMGFLLGAKCI 180  
 OY 181 SCHDCKNK-ECEKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCLASFASVYLACRYORWK 239  
 DB 181 SCNNCKSLKLECKLCPQIENVKGTEDSGTVLLPLVIFGLCLSLFLGLMRYORWK 240  
 OY 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICFSSPSSSPVSIPIYI 290  
 DB 241 SKLYSIVCGKSTPRKEGLEGTGTTKPLAPNPSFSTPGFTPLTGLSPVSSSTFTSSSTYT 300  
 OY 291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350  
 DB 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335  
 OY 351 TPVQKWEASAPASADQADADPATLYAVVGVPPSRMKELVRLGLSEHEIRLELNGR 410  
 DB 336 NPLQKWEBSA-HKQOSLDTDDPATLYAVVENVPPLRKEFVRLGLSDHEIDRLQLONGR 394  
 OY 411 HUREAQSMLAAMRRRTPRREATLELGRVLRMDLGLCLENIEBALGAARLASERPIL 470  
 DB 395 CLREAQYSMLATWRRRTPRREATLELGRVLRMDLGLCLENIEBALGPALPPAPBSLL 454

RESULT 14  
 ID AAB86817 standard; Protein; 455 AA.

XX AC AAB86817;  
 XX DT 12-NOV-2001 (first entry)  
 XX XX Human TNF $\alpha$ -associated protein #1.  
 XX XX TNF $\alpha$ ; tumour necrosis factor binding protein; TNF $\alpha$ ; treatment;  
 KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;  
 KW antiprotocoll; treatment; meningococcal sepsis; cerebral malaria;  
 KW autoimmune glomerulonephritis.  
 XX XX Homo sapiens.  
 XX OS EPI32471-A2.  
 XX PN 12-SEP-2001.  
 XX PD 31-AUG-1990; 2001EP-0108117.  
 XX PF 12-SEP-1989; 88CH-0003319.  
 XX PR 08-MAR-1990; 90CH-0000746.  
 XX PR 20-APR-1990; 90CH-0001347.  
 XX PR 31-AUG-1990; 90EP-0116707.  
 XX PR 31-AUG-1990; 99EP-0100703.  
 XX PA (HOPF ) HOPFMANN LA ROCHE & CO AG F.  
 XX PJ Brockhaue M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;

PI Schlaeger E;  
 XX WPI: 2001-559312/63.  
 DR N-PSDB; AAB48859.

PT New homogeneous, insoluble proteins that bind tumor necrosis factor  
 (TNF), useful for treating TNF-mediated disorders, e.g. inflammation  
 XX Claim 4a; Fig 1; 26pp; German.

CC This invention describes novel insoluble proteins (I), also their  
 CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind  
 CC tumor necrosis factor (TNF) and in homogeneous form. The products of the  
 CC invention have antiinflammatory, immunosuppressive, antibacterial,  
 CC antiprotocoll activity (I), and related recombinant proteins, are used  
 CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal  
 CC sepsis, development of autoimmune glomerulonephritis and cerebral  
 CC malaria. Also (I), or antibodies specific for them, are used for  
 CC diagnostic determination of TNF in body fluids, for affinity purification  
 CC of TNF and for identifying (ant)agonists of TNF. This sequence represents  
 CC a human TNF binding protein described in the method of the invention.

XX Sequence 455 AA;

Query Match 58.3%; Score 1517; DB 22; Length 455;  
 Best Local Similarity 62.9%; Pred. No. 1.4e-95;  
 Matches .302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

OY 1 MGLPTVPGLLPLVLPALLADVPAGVGVLPHPDLEKRESPPQCKYHNPNSTICT 60  
 DB 1 MGLSTVPDLPLPLVLLELVGIVPSGVGLVPHLDREKRSVCPQKGIHPQNNSTICT 60  
 OY 61 KCHKGTVLYNDPCPGPGRDTCRCVCAPGTYTALENHRLRCLSCSRGDEMFWVEISPCVVD 120  
 DB 61 KCHKGTVLYNDPCPGPGRDTCRCVCAPGTYTALENHRLRCLSCSRGDEMFWVEISPCVVD 120  
 OY 121 RDTVCGCRKNQRYRYWSEGTGFRCLNCSLCPNGTINI PCOERODTICHGMGFLLGAKCI 180  
 DB 121 RDTVCGCRKNQRYRYWSEGTGFRCLNCSLCPNGTINI PCOERODTICHGMGFLLGAKCI 180  
 OY 181 SCHDCKNK-ECEKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCLASFASVYLACRYORWK 239  
 DB 181 SCNNCKSLKLECKLCPQIENVKGTEDSGTVLLPLVIFGLCLSLFLGLMRYORWK 240  
 OY 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICFSSPSSSPVSIPIYI 290  
 DB 241 SKLYSIVCGKSTPRKEGLEGTGTTKPLAPNPSFSTPGFTPLTGLSPVSSSTFTSSSTYT 300  
 OY 291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350  
 DB 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335  
 OY 351 TPVQKWEASAPASADQADADPATLYAVVGVPPSRMKELVRLGLSEHEIRLELNGR 410  
 DB 336 NPLQKWEBSA-HKQOSLDTDDPATLYAVVENVPPLRKEFVRLGLSDHEIDRLQLONGR 394  
 OY 411 HUREAQSMLAAMRRRTPRREATLELGRVLRMDLGLCLENIEBALGAARLASERPIL 470  
 DB 395 CLREAQYSMLATWRRRTPRREATLELGRVLRMDLGLCLENIEBALGPALPPAPBSLL 454

RESULT 15  
 ID AAB36697 standard; Protein; 455 AA.

XX AC AAB36697;  
 XX DT 15-MAR-2001 (first entry)  
 XX XX Human tumour necrosis factor receptor TNFR1 protein SEQ ID NO:3.  
 XX XX Human; tumour necrosis factor receptor 5; TR1D; TNFR-5; TR5; neotropic;  
 KW TRAIL receptor without intracellular domain; diagnosis; cytosstatic;

KM tumour necrosis factor related apoptosis inducing ligand; vasotrophic;  
 KM immunosuppressive; neuroprotective; antiviral; antiinflammatory;  
 KM anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
 KM gene therapy; restenosis; graft versus host disease; tumour; cancer;  
 KM apoptotic cell death related disease; autoimmune disorder;  
 KM cardiovascular disorder; viral infection.  
 OS Homo sapiens.  
 FN WO200071150-A1.  
 PD 30-NOV-2000.  
 PE 18-MAY-2000; 2000WO-US3515.  
 PR 20-MAY-1999; 99US-0135164.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Wei Y, Ruben SM, Gentz RL, Ni J;  
 DR WPI; 2001-041051/05.  
 PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor  
 PT necrosis factor receptor 5; useful in the diagnosis, treatment or  
 PT prevention of cancer, autoimmune disorders and viral infection -  
 XX  
 XX  
 PS Disclosure; Fig 2; 285pp; English.  
 CC The present invention describes the human TRID protein (tumour necrosis  
 CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
 CC intracellular domain, also referred to as tumour necrosis factor  
 CC receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,  
 CC neurotropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,  
 CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotrophic  
 CC activities, and can be used in gene therapy. The TRID polynucleotides  
 CC are useful for detecting complementary polynucleotides. TRID proteins and  
 CC polynucleotides are useful in the treatment of tumours, resistance to  
 CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
 CC They are also useful for inducing proliferation of T-cells, endothelial  
 CC cells and certain haematopoietic cells, to regulate antiviral responses  
 CC and to prevent certain autoimmune diseases after stimulation of TRID by  
 CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
 CC polypeptides are useful for treating and/or preventing diseases  
 CC associated with increased or decreased apoptotic cell death. The TRID  
 CC polynucleotides, proteins, antibodies, agonists and antagonists are  
 CC useful in the diagnosis, treatment or prevention of: (a) cancer;  
 CC (b) autoimmune disorders; (c) diseases associated with increased  
 CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The  
 CC present sequence represents a tumour necrosis factor receptor used in  
 CC comparison with TRID in the exemplification of the present invention.  
 CC  
 XX  
 SQ Sequence 455 AA;  
 Query Match 58.3%; Score 1517; DB 22; Length 455;  
 Best Local Similarity 62.9%; Pred. No. 1.4e-95;  
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;  
 QY 1 MGLPTVPGILLPLVLPALLADVYPAGVGLVPHPGDLEKRRSPCPQGGKYNHPONSTICCT 60  
 DB 1 MGLSTVPLDILLPLVLELVGLVIGVPSGVGLVPHLGDREKRDSVCPQGGKTHPNNSTICCT 60  
 QY 61 KCHKGYLYNDCCPGRDPTDRCVACPGTYTALENHLRCLSCSRORDMPQVEISPCVVD 120  
 DB 61 KCHKGYLYNDCCPGRDPTDRCRECESSGFTASENHLRHCLSCSKRKEMGQVEISSCTVD 120  
 QY 121 RDTVCGCRKNQRYRYWGTGTRCLNCSLCPNGCTVNIPOQERODTICGCMGFFLKAKCI 180  
 DB 121 RDTVCGCRKNQRYRYWSENLPQCFCNCSLCLNGTVHLSQCKRQNTVCTCHAGFFLRNECV 180  
 QY 181 SCHDCKNK-ECEKLCPTFPSTGSDODPGTTLVLPVIVFGLCLASPASVYLACRYORWK 239  
 DB 181 SCNNCKSLKCTKCLPQIENVKGTEDSGTTLVLPVIVFGLCLSLFLGLMTRYORWK 240

QY 240 PKLYSIICGOSTLVKEGEP-----LIVPAGFNP-----TTTICFSSSTPSSSPVISIPPYI 290  
 DB 241 SKLYSIVCGKSTPERKEGLEGTTKPLAPNPSFPTGFTPLGFSVPVPSSTFTSSSYT 300  
 QY 291 SCDSNNGAVASPSSETPAPPLKAGPILPCGPASTHLCTGPPASTHLCTGPPASTHLCT 350  
 DB 301 PGDCPNF---AAPREVAAPPYOGADPIL-----ATAL-----ASDPPI 335  
 QY 351 TPVOKWEASAPSDOLADADPATLVAVDGPVPSRKELVRRGLSEHEIERLENGR 410  
 DB 336 NPLQKMEDSA-HKQSLDTPDLPATLVAVENVPPLRKKEFRRLGLSDHEIDRELQNGR 394  
 QY 411 HLRBAQYSMLAAMRRTPREATLLELGRVLRDMDLGCLENIEEALGAARLASBPRL 470  
 DB 395 CLREAQYSMLATWRRTPREATLELGRVLRDMDLGCLIEDIEEALGAPALPPAPSL 454

Search completed: September 13, 2003, 07:04:10  
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OM protein - protein search, using sw model

Run on: September 13, 2003, 07:03:14 ; Search time 21 Seconds

(without alignments)  
948.972 Million cell updates/sec

Title: US-09-970-532-2

Perfect score: 2603 1 MGLPTVGGLLPLVPLALIA.....NIEALGAGARLASEPRLW 471

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1519	58.4	455	1	US-08-406-824A-4
3	1517	58.3	455	1	US-08-321-668-2
4	1517	58.3	455	1	US-08-837-941-2
5	1517	58.3	455	2	US-08-126-016-2
6	1517	58.3	455	3	US-08-815-469-5
7	1517	58.3	455	3	US-09-006-353A-3
8	1517	58.3	455	4	US-09-527-236A-5
9	1517	58.3	455	4	US-08-054-970-2
10	1517	58.3	455	4	US-09-565-918-4
11	1517	58.3	455	4	US-09-573-986-3
12	1517	58.3	455	4	US-09-027-287-3
13	1517	58.3	455	1	US-09-253-656B-3
14	1512	58.1	455	1	US-08-050-319B-25
15	1512	58.1	455	2	US-08-465-982-25
16	1500.5	57.6	909	4	US-09-013-895A-4
17	1500.5	57.6	909	4	US-09-448-868-4
18	1496	57.5	453	4	US-09-086-483A-5
19	1496	57.5	453	4	US-09-580-212-5
20	1423	54.7	426	4	US-08-747-562-37
21	1072	41.2	181	4	US-09-513-007-4
22	1019	39.1	280	3	US-08-974-022-46
23	1019	39.1	280	3	US-08-795-445A-46
24	1019	39.1	280	3	US-08-795-447A-46
25	1019	39.1	280	3	US-08-974-186-46
26	1019	39.1	280	3	US-08-795-446B-46
27	1019	39.1	280	4	US-08-706-945D-132

28	813.5	31.3	197	4	US-08-828-683A-21	Sequence 21, Appli
29	807.5	31.0	199	1	US-08-050-319B-48	Sequence 48, Appli
30	807.5	31.0	199	2	US-08-465-982-48	Sequence 48, Appli
31	727.5	27.9	336	3	US-08-804-166-8	Sequence 8, Appli
32	727.5	27.9	336	3	US-08-910-991-8	Sequence 8, Appli
33	719	27.6	167	1	US-08-050-319B-2	Sequence 2, Appli
34	719	27.6	167	1	US-08-050-319B-57	Sequence 57, Appli
35	719	27.6	167	2	US-08-465-982-2	Sequence 2, Appli
36	719	27.6	167	2	US-08-465-982-57	Sequence 57, Appli
37	680.5	26.1	285	3	US-08-804-166-6	Sequence 6, Appli
38	680.5	26.1	285	3	US-08-910-991-6	Sequence 6, Appli
39	679	26.1	307	3	US-08-804-166-4	Sequence 4, Appli
40	679	26.1	307	3	US-08-910-991-4	Sequence 4, Appli
41	674.5	25.9	161	4	US-09-326-394-2	Sequence 2, Appli
42	670.5	25.8	153	2	US-08-219-237B-4	Sequence 4, Appli
43	670.5	25.8	153	3	US-08-477-347-12	Sequence 12, Appli
44	670.5	25.8	153	3	US-08-476-862-3	Sequence 3, Appli
45	670.5	25.8	153	3	US-08-468-560C-4	Sequence 4, Appli

## ALIGNMENTS

```

RESULT 1
US-09-513-007-2
; Sequence 2, Application US/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrl, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/513,007
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/122,156
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-513-007-2

Query Match      100.0%; Score 2603; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 5.6e-197;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLPTVGGLLPLVPLALIAADVYPAGVQGLVPHPGDLEKESPCQCKYHHPNSTICT 60
DB 1 MGLPTVGGLLPLVPLALIAADVYPAGVQGLVPHPGDLEKESPCQCKYHHPNSTICT 60
QY 61 KCHKGTLYNDPCPGADTDCRVCAFGTYALENHLRCLSCSRRGEMOVEISPCVVD 120
DB 61 KCHKGTLYNDPCPGADTDCRVCAFGTYALENHLRCLSCSRRGEMOVEISPCVVD 120
QY 121 RDTVCGGRKQVREYMGDTGFRCLNCSLCPNGTVNI PCQERODTICHGNGFLKAKCI 180
DB 121 RDTVCGGRKQVREYMGDTGFRCLNCSLCPNGTVNI PCQERODTICHGNGFLKAKCI 180
QY 181 SCHDCKRKECKICPRPSTGKSDODGTIVLLPLVVFGLCLASFASVYLACRYQWKP 240
DB 181 SCHDCKRKECKICPRPSTGKSDODGTIVLLPLVVFGLCLASFASVYLACRYQWKP 240
QY 241 KLVSIIGQSTLVKEGPELVLPAPGNPTTICFSSPSSPVSIPIPYISCDRSNFGAV 300
DB 241 KLVSIIGQSTLVKEGPELVLPAPGNPTTICFSSPSSPVSIPIPYISCDRSNFGAV 300
QY 301 ASRSGTAPHLKAGPLPGPPASTHLCTGPPASTHLCTGPPASTHLCTPVQKWEASA 360
DB 301 ASRSGTAPHLKAGPLPGPPASTHLCTGPPASTHLCTGPPASTHLCTPVQKWEASA 360

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Db 301 ASPSETAPPHLKAGPILEGPASTHLCCTPPASTHLCCTPPASTHLCCTPPVQKWEASA 360  
Qy 361 PSAPQGLADADPATYAVVDGVPSPRMEKELVRRLGLSEHEIERLENGRHLREAOYQML 420  
Db 361 PSAPQGLADADPATYAVVDGVPSPRMEKELVRRLGLSEHEIERLENGRHLREAOYQML 420  
Qy 421 AAMRRTRRREATELLEGRVLRDMDLGCLLENIEBALGGAARLASERPLW 471  
Db 421 AAMRRTRRREATELLEGRVLRDMDLGCLLENIEBALGGAARLASERPLW 471

## RESULT 2

US-08-406-824A-4  
Sequence 4, Application US/08406824A  
Patent No. 6541610  
GENERAL INFORMATION:  
APPLICANT: SMITH, Craig A.  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS  
FILE REFERENCE: A-71592  
CURRENT APPLICATION NUMBER: US/08/406,824A  
CURRENT FILING DATE: 1995-03-20  
PRIOR APPLICATION NUMBER: US 08/255,849  
PRIOR FILING DATE: 1994-06-08  
PRIOR APPLICATION NUMBER: US 07/860,710  
PRIOR FILING DATE: 1992-03-30  
PRIOR APPLICATION NUMBER: US 07/523,635  
PRIOR FILING DATE: 1990-05-10  
PRIOR APPLICATION NUMBER: US 07/421,417  
PRIOR FILING DATE: 1989-10-13  
PRIOR APPLICATION NUMBER: US 07/405,370  
PRIOR FILING DATE: 1989-09-11  
PRIOR APPLICATION NUMBER: US 07/403,241  
PRIOR FILING DATE: 1988-09-05  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-406-824A-4

Query Match 58.4%; Score 1519; DB 4; Length 455;  
Best Local Similarity 62.9%; Pred. No. 1e-111;  
Matches 302; Conservative 39; Mismatches 103; Indels 36; Gaps 7;

Qy 1 MGLPTVPGILLPLVLPALLADYPRAGVGLVPHPGDLKRESPCCQKKNHQNSTICT 60  
Db 1 MGLSTVPDLLPLVLLELVGIYPSGVIGLVPHLDREKRDVCPQGXIHPONNISICT 60  
Qy 61 KCHKGTLYLNDPCPGRDTCRVCAAGTYTALLENHLRCLSCSRDEMFQVEISPCVVD 120  
Db 61 KCHKGTLYLNDPCPGRDTCRVCAAGTYTALLENHLRCLSCSRDEMFQVEISPCVVD 120  
Qy 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCOERODIT CHCHMGFFLKGAACI 180  
Db 121 RDTVCGCRKNQYRHVMSBNLFCFCFNCISCLNGTVHLSCEKKNYCTGAGFFLENECV 180  
Qy 181 SCHDCKNK-ECEKLCPTPSTGKSODPGTTVLLPLVIVFGICLASFASVVLACYQRWK 239  
Db 181 SCHDCKNK-ECEKLCPTPSTGKSODPGTTVLLPLVIVFGICLASFASVVLACYQRWK 239  
Qy 240 PLYYSIIICGOSTLVKEGPE-----LLVAPAGFNP-----TTTICSPSTSSSPVSIPIYI 290  
Db 240 PLYYSIIICGOSTLVKEGPE-----LLVAPAGFNP-----TTTICSPSTSSSPVSIPIYI 290  
Qy 291 SCDRSNFGAVASPSSETAPPHLKAGPILEGPASTHLCCTPPASTHLCCTPPASTHLC 350  
Db 301 PGDCRNF---AARREVAAPYOGADPIL-----ATL-----ASDPIP 335  
Qy 351 TVQKWEASAPAPQGLADADPATYAVVDGVPSPRMEKELVRRLGLSEHEIERLENGR 410  
Db 336 NPLQKWEBSA-HKPGGLDTPDDPATYAVVENVPPLRWKEFVRLGLSDHEIDRLLENGR 394

Qy 411 HIREAOYSMLAAMRRTRRREATELLEGRVLRDMDLGCLLENIEBALGGAARLASERPL 470  
Db 395 CLRAOYSMLATWRTRRTRRREATELLEGRVLRDMDLGCLLENIEBALGGAARLASERPL 454

## RESULT 3

US-08-321-668-2  
Sequence 2, Application US/08321668  
Patent No. 565859  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
APPLICANT: VARELOMEYEV, Eugene  
APPLICANT: BATKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/321,668  
FILING DATE: 12-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH-13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-321-668-2

Query Match 58.3%; Score 1517; DB 1; Length 455;  
Best Local Similarity 62.9%; Pred. No. 1.5e-111;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPGILLPLVLPALLADYPRAGVGLVPHPGDLKRESPCCQKKNHQNSTICT 60  
Db 1 MGLSTVPDLLPLVLLELVGIYPSGVIGLVPHLDREKRDVCPQGXIHPONNISICT 60  
Qy 61 KCHKGTLYLNDPCPGRDTCRVCAAGTYTALLENHLRCLSCSRDEMFQVEISPCVVD 120  
Db 61 KCHKGTLYLNDPCPGRDTCRVCAAGTYTALLENHLRCLSCSRDEMFQVEISPCVVD 120  
Qy 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCOERODIT CHCHMGFFLKGAACI 180  
Db 121 RDTVCGCRKNQYRHVMSBNLFCFCFNCISCLNGTVHLSCEKKNYCTGAGFFLENECV 180  
Qy 181 SCHDCKNK-ECEKLCPTPSTGKSODPGTTVLLPLVIVFGICLASFASVVLACYQRWK 239  
Db 181 SCHDCKNK-ECEKLCPTPSTGKSODPGTTVLLPLVIVFGICLASFASVVLACYQRWK 239  
Qy 240 PLYYSIIICGOSTLVKEGPE-----LLVAPAGFNP-----TTTICSPSTSSSPVSIPIYI 290  
Db 240 PLYYSIIICGOSTLVKEGPE-----LLVAPAGFNP-----TTTICSPSTSSSPVSIPIYI 290

Db 241 SKLSIVCGSKTPEKEGELGTTTKPLAPNPSFSTPGFTPLTGGSPVSSSTFTSSSTYT 300  
Qy 291 SCDSNFGAVASPSSETPAPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350  
Db 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATL-----ASDPIP 335  
Qy 351 TPVOKWEASAPSDOLADADPATLYAVVDGVPSPRWKELVRLGSEHEIERLEENGR 410  
Db 336 NPLQKMEDSA-HKPOSIDTDDPATLYAVVENPPRLRWKEFVRRLGSDHEIDRLLEQNGR 394  
Qy 411 HREAOYSMLAAMRRTPREATTELIGRVLARMDDLGCLENIEBALGGAARLASEBRL 470  
Db 395 CLRBAQYSMLATWRRTPRREATTELIGRVLARMDDLGCLEDBALCGPALPPAPSL 454

RESULT 4  
US-08-837-941-2  
Sequence 2, Application US/08837941  
Patent No. 576917

GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
APPLICANT: VARPOLOMEY, Eugene  
APPLICANT: BARKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,941  
FILING DATE: 28-APR-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/321,668  
FILING DATE: 12-OCT-1994  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528

TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-837-941-2

Query Match 58.3%; Score 1517; DB 1; Length 455;  
Best Match Similarity 62.9%; Pred. No. 1.5e-11;  
Matches 302; Conservative 36; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPGALLPLVPLALLADVPAGVGLVPHPGDLEKESPCQCKYNNPQNSTICTCT 60  
Db 1 MGLSTVPDLLPLVPLVLLVGLVYSVIGLVPHLGRKSDSVQCKYIHPQNSICTCT 60

Qy 61 KCHKGYLVNDCCPGRDTDCRVACPGTYTALENHLRCLSCGRCDMEFQVEISPCVVD 120  
Db 61 KCHKGYLVNDCCPGRDTDCRVACPGTYTALENHLRCLSCGRCDMEFQVEISPCVVD 120  
Qy 121 RDTVCGGRKQYRYRWKETGRCLNCSLCPNGTYNINICQSRDOTTICCHNGFFLKAKCI 180  
Db 121 RDTVCGGRKQYRYRWSENFQCFNCCLCUNGTVHLSQCKQNTVCTCHAGFFIRENECV 180  
Qy 181 SCHDCKRK-SCENKLCFPRSTGKDSODPGTTVLLPLVTVGLCLASAVVLAQRYRWK 239  
Db 181 SCNCKSLSECTHCLCPQIENVKTEBDSGTVLLPLVTFGLCLSLFGLMRYRWK 240  
Qy 240 PKLYSIICGOSTLVKEGPE-----LLVPAGFNP-----TTTCFSSTPSSPVSIPIYI 290  
Db 241 SKLSIVCGSKTPEKEGELGTTTKPLAPNPSFSTPGFTPLTGGSPVSSSTFTSSSTYT 300  
Qy 291 SCDSNFGAVASPSSETPAPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350  
Db 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATL-----ASDPIP 335  
Qy 351 TPVOKWEASAPSDOLADADPATLYAVVDGVPSPRWKELVRLGSEHEIERLEENGR 410  
Db 336 NPLQKMEDSA-HKPOSIDTDDPATLYAVVENPPRLRWKEFVRRLGSDHEIDRLLEQNGR 394  
Qy 411 HREAOYSMLAAMRRTPREATTELIGRVLARMDDLGCLENIEBALGGAARLASEBRL 470  
Db 395 CLRBAQYSMLATWRRTPRREATTELIGRVLARMDDLGCLEDBALCGPALPPAPSL 454

RESULT 5  
US-08-126-016-2  
Sequence 2, Application US/08126016  
Patent No. 581261

GENERAL INFORMATION:  
APPLICANT: WALLACH, DAVID  
APPLICANT: NODAR, YARON  
APPLICANT: KEMPER, OLIVER  
APPLICANT: ENGELMANN, HARTMUT  
APPLICANT: BRAKEBUSCH, CORD  
APPLICANT: ADERKA, DAN  
TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TNF-I)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street, N.W., Suite 300.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/126,016  
FILING DATE: 24-SEP-1993  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/625668  
FILING DATE: 13-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528

TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-126-016-2

Query Match 58.3%; Score 1517; DB 2; Length 455;  
Best Local Similarity 62.9%; Pred. No. 1.5e-111;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPLLLPLVLPALLADVPAGVGLVPHPDLEKRESPPCQKYNHPONSTICT 60  
DB 1 MGLSTVPDLLPLVLELVGLVIGVSGVIGLVPHLDREKRUSVCPQKTIHPONNSICT 60  
QY 61 KCHKGTLYLNDPCPGQDTPDCRECESSGFTASENHLRCLSCSKCKRMGVETISSCTVD 120  
DB 61 KCHKGTLYLNDPCPGQDTPDCRECESSGFTASENHLRCLSCSKCKRMGVETISSCTVD 120  
QY 121 RDTVCGCRKNQYREYWGTEGFRCLNCSLCPNGTVNIPCEQRODITCHCHMGFFLGAKCI 180  
DB 121 RDTVCGCRKNQYRHMYSENLPCFCNCSLCNCTVHLSQCEKQNTVCTCHAGFFLENECV 180  
QY 181 SCHDCKN-ECEKLCPTRPSTGKSDQDGTTLPLVIVFGCLCLASFASVVLACYORK 239  
DB 181 SCNCKKSLKCTKCLPQIENKGTEDSGTTLPLVIFGCLCLSLFGLMRYQRMK 240  
QY 240 PKLYSIICGOSTLVKEGEPE-----LVVAPGFNP-----TTTICFSSSTPSSPVSIPIYI 290  
DB 241 SKLYSIVCGKSTPEKEGELGTTTKPLANPSFSPTPGFTPLGSPVPSSTFTSSSTYT 300  
QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCPPGPASTHLCPPGPASTHLC 350  
DB 301 PGDCPNF---AAPRREVAAPYOGADPIL-----ATAL-----ASDPIP 335  
QY 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPKWEKLVRLGLSHEIERLENGR 410  
DB 336 NPLQKWEBSA-HKPSLTDTPATLYAVVENVPPLRKEFVRLGLSHEIERLENGR 394  
QY 411 HUREAOSMLAAMRRTPRREATTLELGRVLRDMDLGLCLENIEBALGAARLASEPRL 470  
DB 395 CUREAOSMLATWRRTPRREATTLELGRVLRDMDLGLCLENIEBALGPALPAPPSIL 454

## RESULT 6

US-08-815-469-5  
Sequence 5, Application US/08815469  
Patent No. 6153402  
GENERAL INFORMATION:  
APPLICANT: YU, GUO-LIANG  
APPLICANT: NI, JIAN  
APPLICANT: DIXIE, VIASHA  
APPLICANT: GENTZ, REINER L.  
APPLICANT: DILLON, PATRICK J.  
TITLE OF INVENTION: Death Domain Containing Receptors  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., NW, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/815,469  
FILING DATE: HEREWITH  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NO. 6153402 Yet Assigned  
FILING DATE: 06-FEB-1997

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/028,711  
FILING DATE: 17-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/013,285  
FILING DATE: 12-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-815-469-5

Query Match 58.3%; Score 1517; DB 3; Length 455;  
Best Local Similarity 62.9%; Pred. No. 1.5e-111;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

QY 1 MGLPTVPLLLPLVLPALLADVPAGVGLVPHPDLEKRESPPCQKYNHPONSTICT 60  
DB 1 MGLSTVPDLLPLVLELVGLVIGVSGVIGLVPHLDREKRUSVCPQKTIHPONNSICT 60  
QY 61 KCHKGTLYLNDPCPGQDTPDCRECESSGFTASENHLRCLSCSKCKRMGVETISSCTVD 120  
DB 61 KCHKGTLYLNDPCPGQDTPDCRECESSGFTASENHLRCLSCSKCKRMGVETISSCTVD 120  
QY 121 RDTVCGCRKNQYREYWGTEGFRCLNCSLCPNGTVNIPCEQRODITCHCHMGFFLGAKCI 180  
DB 121 RDTVCGCRKNQYRHMYSENLPCFCNCSLCNCTVHLSQCEKQNTVCTCHAGFFLENECV 180  
QY 181 SCHDCKN-ECEKLCPTRPSTGKSDQDGTTLPLVIVFGCLCLASFASVVLACYORK 239  
DB 181 SCNCKKSLKCTKCLPQIENKGTEDSGTTLPLVIFGCLCLSLFGLMRYQRMK 240  
QY 240 PKLYSIICGOSTLVKEGEPE-----LVVAPGFNP-----TTTICFSSSTPSSPVSIPIYI 290  
DB 241 SKLYSIVCGKSTPEKEGELGTTTKPLANPSFSPTPGFTPLGSPVPSSTFTSSSTYT 300  
QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCPPGPASTHLCPPGPASTHLC 350  
DB 301 PGDCPNF---AAPRREVAAPYOGADPIL-----ATAL-----ASDPIP 335  
QY 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPKWEKLVRLGLSHEIERLENGR 410  
DB 336 NPLQKWEBSA-HKPSLTDTPATLYAVVENVPPLRKEFVRLGLSHEIERLENGR 394  
QY 411 HUREAOSMLAAMRRTPRREATTLELGRVLRDMDLGLCLENIEBALGAARLASEPRL 470  
DB 395 CUREAOSMLATWRRTPRREATTLELGRVLRDMDLGLCLENIEBALGPALPAPPSIL 454

## RESULT 7

US-09-006-353A-3  
Sequence 3, Application US/09006353A  
Patent No. 6261801  
GENERAL INFORMATION:  
APPLICANT: WEI, YING-FEI  
APPLICANT: YU, GUO-LIANG  
APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006.353A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A  
REGISTRATION NUMBER: 36.373  
REFERENCE/DOCKET NUMBER: P3741  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-006-353A-3

Query Match 58.3%; Score 1517; DB 3; Length 455;  
Best Local Similarity 62.9%; Pred. No. 1.5e-111;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;  
QY 1 MGLPTVPGLLPLVLPALLADVPAGVGVHPHGDLEKRESPPCGKYNHNSICTCT 60  
DB 1 MGLSTVPGLLPLVLPALLADVPAGVGVHPHGDLEKRESPPCGKYNHNSICTCT 60  
QY 61 KCHKGTLYNDPCPGRDTCRCVCAAGTYTALENHRLRCLSCSRDEMFVEISPCVVD 120  
DB 61 KCHKGTLYNDPCPGRDTCRCVCAAGTYTALENHRLRCLSCSRDEMFVEISPCVVD 120  
QY 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMGFLKAGACI 180  
DB 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMGFLKAGACI 180  
QY 181 SCHDCNKN-ECEKLCPTPSTGKSDODPGTTLPLVIVFGICLASFASVYLACRYORWK 239  
DB 181 SCHDCNKN-ECEKLCPTPSTGKSDODPGTTLPLVIVFGICLASFASVYLACRYORWK 239  
QY 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTCFSSTPSSSPVISIPYI 290  
DB 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTCFSSTPSSSPVISIPYI 290  
QY 301 PDGDCPNF---AAPRREVPAPYOGADPIL-----ATL-----ASDPIP 335  
DB 301 PDGDCPNF---AAPRREVPAPYOGADPIL-----ATL-----ASDPIP 335  
QY 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRGLSHEIERLENGR 410  
DB 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRGLSHEIERLENGR 410  
QY 394 411 HLEAQQSMLAAMRRRTPREATLELGRVLRDMDLGCLNIEBALGAARLASEPRLL 470  
DB 394 411 HLEAQQSMLAAMRRRTPREATLELGRVLRDMDLGCLNIEBALGAARLASEPRLL 470  
QY 395 CLREAOYSMLATWRRRTPREATLELGRVLRDMDLGCLNIEBALGAARLASEPRLL 454  
DB 395 CLREAOYSMLATWRRRTPREATLELGRVLRDMDLGCLNIEBALGAARLASEPRLL 454

RESULT 8  
US-09-527-236A-5  
Sequence 5, Application US/09527236A  
Patent No. 6358508  
GENERAL INFORMATION:  
APPLICANT: NI, Jian  
APPLICANT: Yu, Guo-Liang

APPLICANT: Fan, Ping  
APPLICANT: Gentz, Reiner L.  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
FILE REFERENCE: P375P1  
CURRENT APPLICATION NUMBER: US/09/527.236A  
PRIOR FILING DATE: 2000-03-16  
PRIOR APPLICATION NUMBER: 60/052,991  
PRIOR FILING DATE: 1997-06-11  
PRIOR APPLICATION NUMBER: 09/095,094  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/126,019  
PRIOR FILING DATE: 1999-03-24  
PRIOR APPLICATION NUMBER: 60/134,220  
PRIOR FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-527-236A-5

Query Match 58.3%; Score 1517; DB 4; Length 455;  
Best Local Similarity 62.9%; Pred. No. 1.5e-111;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;  
QY 1 MGLPTVPGLLPLVLPALLADVPAGVGVHPHGDLEKRESPPCGKYNHNSICTCT 60  
DB 1 MGLSTVPGLLPLVLPALLADVPAGVGVHPHGDLEKRESPPCGKYNHNSICTCT 60  
QY 61 KCHKGTLYNDPCPGRDTCRCVCAAGTYTALENHRLRCLSCSRDEMFVEISPCVVD 120  
DB 61 KCHKGTLYNDPCPGRDTCRCVCAAGTYTALENHRLRCLSCSRDEMFVEISPCVVD 120  
QY 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMGFLKAGACI 180  
DB 121 RDTVCGCKNQYREHWGTGFRCLNCSLCPNGTVNIPCOERODTICHGMGFLKAGACI 180  
QY 181 SCHDCNKN-ECEKLCPTPSTGKSDODPGTTLPLVIVFGICLASFASVYLACRYORWK 239  
DB 181 SCHDCNKN-ECEKLCPTPSTGKSDODPGTTLPLVIVFGICLASFASVYLACRYORWK 239  
QY 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTCFSSTPSSSPVISIPYI 290  
DB 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTCFSSTPSSSPVISIPYI 290  
QY 301 PDGDCPNF---AAPRREVPAPYOGADPIL-----ATL-----ASDPIP 335  
DB 301 PDGDCPNF---AAPRREVPAPYOGADPIL-----ATL-----ASDPIP 335  
QY 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRGLSHEIERLENGR 410  
DB 351 TPVQKWEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRGLSHEIERLENGR 410  
QY 394 411 HLEAQQSMLAAMRRRTPREATLELGRVLRDMDLGCLNIEBALGAARLASEPRLL 470  
DB 394 411 HLEAQQSMLAAMRRRTPREATLELGRVLRDMDLGCLNIEBALGAARLASEPRLL 470  
QY 395 CLREAOYSMLATWRRRTPREATLELGRVLRDMDLGCLNIEBALGAARLASEPRLL 454  
DB 395 CLREAOYSMLATWRRRTPREATLELGRVLRDMDLGCLNIEBALGAARLASEPRLL 454

RESULT 9  
US-08-054-970-2  
Sequence 2, Application US/08054970  
Patent No. 6395267  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKESBUSH, Cord  
TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W.  
CITY: Washington  
STATE: D.C.

```

/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/06/054,970
/ FILING DATE: 03-MAY-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: WALLACH=9
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 455 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-054-970-2

```

```

Query Match      58.3%; Score 1517; DB 4; Length 455;
Beet Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGKYNHPONSTICT 60
DB 1 MGLSTVPLDLPLVLELVGLVPSGVIGLVPHLDREGRDVSVCQKTIHPQNNSTICT 60
QY 61 KHKGTLYNDPCPGGRDTCRCVCAPTYTALLENHRLRCLSCSRCDMPQVEISPCVVD 120
DB 61 KHKGTLYNDPCPGGRDTCRCVCAPTYTALLENHRLRCLSCSRCDMPQVEISPCVVD 120
QY 121 RDTVCGCRKNQRYRYWSENLFCFNCISLCNGTVHLSCEKONTVCTCHAGFPLENRCV 180
DB 121 RDTVCGCRKNQRYRYWSENLFCFNCISLCNGTVHLSCEKONTVCTCHAGFPLENRCV 180
QY 181 SCHDCKNK-ECEKLCPTPSTGKDSODPGTTLPLVIVFGLCLASFASVVLACRYQWK 239
DB 181 SCHDCKNK-ECEKLCPTPSTGKDSODPGTTLPLVIVFGLCLASFASVVLACRYQWK 239
QY 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICFSSSTPSSPVSIPIYI 290
DB 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICFSSSTPSSPVSIPIYI 290
QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCCTPPASTHLCCTPPASTHLC 350
DB 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCCTPPASTHLCCTPPASTHLC 350
QY 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPIP 335
DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPIP 335
QY 351 TPVQKWEASAPSAPODLADADPATLYAVVDGVPSPRWKELVRLGLSHEIERLELENGR 410
DB 351 TPVQKWEASAPSAPODLADADPATLYAVVDGVPSPRWKELVRLGLSHEIERLELENGR 410
QY 336 NPLOQWEDSA-HKPSQSLDTPDPAITLYAVENVPLRWKEFPVRLGLSDHEIDRLLEONGR 394
DB 336 NPLOQWEDSA-HKPSQSLDTPDPAITLYAVENVPLRWKEFPVRLGLSDHEIDRLLEONGR 394
QY 411 HLREAOYSMLAAMRRTPRREATLELLGRVLRMDMLGCLLENIEBALGGAARLASERPLL 470
DB 411 HLREAOYSMLAAMRRTPRREATLELLGRVLRMDMLGCLLENIEBALGGAARLASERPLL 470
QY 395 CLREAOYSMLATWRRTPRREATLELLGRVLRMDMLGCLLENIEBALGGAARLASERPLL 454
DB 395 CLREAOYSMLATWRRTPRREATLELLGRVLRMDMLGCLLENIEBALGGAARLASERPLL 454

```

RESULT 10  
US-09-565-918-4

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/ Sequence 4, Application US/09565918
/ Patent No. 6433147
/ GENERAL INFORMATION:
/ APPLICANT: NI, Jian
/ APPLICANT: Roosen, Craig A.
/ APPLICANT: Pan, James G.
/ APPLICANT: Gentz, Reiner L.

```

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/ APPLICANT: Dixit, Vishva M.
/ TITLE OF INVENTION: Death Domain Containing Receptor 4
/ FILE REFERENCE: 1488.130005
/ CURRENT APPLICATION NUMBER: US/09/565,918
/ CURRENT FILING DATE: 2000-05-05
/ PRIOR APPLICATION NUMBER: US 60/132,922
/ PRIOR FILING DATE: 1999-05-06
/ PRIOR APPLICATION NUMBER: US 09/013,895
/ PRIOR FILING DATE: 1998-01-27
/ PRIOR APPLICATION NUMBER: US 60/037,829
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: US 60/035,722
/ PRIOR FILING DATE: 1997-01-28
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-565-918-4

```

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Query Match      58.3%; Score 1517; DB 4; Length 455;
Beet Local Similarity 62.9%; Pred. No. 1.5e-111;
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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QY 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGKYNHPONSTICT 60
DB 1 MGLSTVPLDLPLVLELVGLVPSGVIGLVPHLDREGRDVSVCQKTIHPQNNSTICT 60
QY 61 KHKGTLYNDPCPGGRDTCRCVCAPTYTALLENHRLRCLSCSRCDMPQVEISPCVVD 120
DB 61 KHKGTLYNDPCPGGRDTCRCVCAPTYTALLENHRLRCLSCSRCDMPQVEISPCVVD 120
QY 121 RDTVCGCRKNQRYRYWSENLFCFNCISLCNGTVHLSCEKONTVCTCHAGFPLENRCV 180
DB 121 RDTVCGCRKNQRYRYWSENLFCFNCISLCNGTVHLSCEKONTVCTCHAGFPLENRCV 180
QY 181 SCHDCKNK-ECEKLCPTPSTGKDSODPGTTLPLVIVFGLCLASFASVVLACRYQWK 239
DB 181 SCHDCKNK-ECEKLCPTPSTGKDSODPGTTLPLVIVFGLCLASFASVVLACRYQWK 239
QY 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICFSSSTPSSPVSIPIYI 290
DB 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICFSSSTPSSPVSIPIYI 290
QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCCTPPASTHLCCTPPASTHLC 350
DB 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCCTPPASTHLCCTPPASTHLC 350
QY 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPIP 335
DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPIP 335
QY 351 TPVQKWEASAPSAPODLADADPATLYAVVDGVPSPRWKELVRLGLSHEIERLELENGR 410
DB 351 TPVQKWEASAPSAPODLADADPATLYAVVDGVPSPRWKELVRLGLSHEIERLELENGR 410
QY 336 NPLOQWEDSA-HKPSQSLDTPDPAITLYAVENVPLRWKEFPVRLGLSDHEIDRLLEONGR 394
DB 336 NPLOQWEDSA-HKPSQSLDTPDPAITLYAVENVPLRWKEFPVRLGLSDHEIDRLLEONGR 394
QY 411 HLREAOYSMLAAMRRTPRREATLELLGRVLRMDMLGCLLENIEBALGGAARLASERPLL 470
DB 411 HLREAOYSMLAAMRRTPRREATLELLGRVLRMDMLGCLLENIEBALGGAARLASERPLL 470
QY 395 CLREAOYSMLATWRRTPRREATLELLGRVLRMDMLGCLLENIEBALGGAARLASERPLL 454
DB 395 CLREAOYSMLATWRRTPRREATLELLGRVLRMDMLGCLLENIEBALGGAARLASERPLL 454

```

RESULT 11  
US-09-573-986-3

```

/ Sequence 3, Application US/09573986
/ Patent No. 6455040
/ GENERAL INFORMATION:
/ APPLICANT: Wei, Ying-Fei
/ APPLICANT: NI, Jian
/ APPLICANT: Gentz, Reiner
/ APPLICANT: Ruben, Steven
/ TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
/ FILE REFERENCE: 1488.1280004
/ CURRENT APPLICATION NUMBER: US/09/573,986
/ CURRENT FILING DATE: 2000-05-18
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: Patentin Ver. 2.1

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SEQ ID NO 3  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-573-986-3

Query Match 58.3%; Score 1517; DB 4; Length 455;  
Best Local Similarity 62.9%; Pred. No. 1.5e-111;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

1 MGLPTVPLLLPLVLPALLADVPAGVQGLVPHGDLKRESPPQKQKYNPNSTICT 60  
1 MGLSTVPLLLPLVLLBLVIGIYPSGVGLVPHGLDKRSDVCPQKXIHPONNISICT 60  
61 KCHKGTLYNDPCPGRDTRCVACPTTYALLENHRLRCLSCSRGRDMPFVIEISPCVVD 120  
61 KCHKGTLYNDPCPGRDTRCVACPTTYALLENHRLRCLSCSRGRDMPFVIEISPCVVD 120  
121 RDTVCGCKNOYREYWGTRCLNCSLCFNGTNNI PCOEKODTICHGMGFLKAGACI 180  
121 RDTVCGCKNOYREYWGTRCLNCSLCFNGTNNI PCOEKODTICHGMGFLKAGACI 180  
121 RDTVCGCKNOYREYWGTRCLNCSLCFNGTNNI PCOEKODTICHGMGFLKAGACI 180  
181 SCHDCKNK-ECCKLCPTPSTGKSDODPDTTLLPLVIFGLCLASFASVVLACRYGRMK 239  
181 SCHDCKNK-ECCKLCPTPSTGKSDODPDTTLLPLVIFGLCLASFASVVLACRYGRMK 239  
181 SCHDCKNK-ECCKLCPTPSTGKSDODPDTTLLPLVIFGLCLASFASVVLACRYGRMK 239  
240 PKLYSIICGOSTLYKEGEP-LLVPAGFNP-TTTCFSSTPSSSPVSIIPYI 290  
241 SKLYSIVCGKSTPEKEGELBGTTRKPLAPNPSFPTPGFTPLGFSVPSSSTFTSSYTT 300  
291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350  
301 PGDCPNF---AAPREVAAPYOGADPIL-----ATAL-----ASDPIP 335  
351 TPVQKESASAPADQLADADPATLYAVADGVPSPRWELVRILGSLSEHIERLENGR 410  
336 NPLQKMEISA-HKQSLDTPDPAITYAVENVPLRWKPEFARRGLSHEIDRLQLQNGR 394  
411 HLEAQSMLAAMRRRTPRREATTLELLGRVLRDMDLGCLLENIBALGAARLASEPRL 470  
395 CLREAQYMLATWRRRTPRREATTLELLGRVLRDMDLGCLLENIBALGAARLASEPRL 454

RESULT 12  
US-09-027-287-3  
Sequence 3, Application US/09027287A  
Patent No. 6479254  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M.  
APPLICANT: Ullrich, Stephen  
TITLE OF INVENTION: Apoptosis Inducing Molecule II  
FILE REFERENCE: 1488.0650004  
CURRENT APPLICATION NUMBER: US/09/027,287A  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 09/003,886  
PRIOR FILING DATE: 1998-01-07  
PRIOR APPLICATION NUMBER: US 08/822,953  
PRIOR FILING DATE: 1997-03-21  
PRIOR APPLICATION NUMBER: US 60/030,157  
PRIOR FILING DATE: 1996-10-31  
PRIOR APPLICATION NUMBER: US 60/013,923  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-027-287-3

Query Match 58.3%; Score 1517; DB 4; Length 455;

Best Local Similarity 62.9%; Pred. No. 1.5e-111;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

1 MGLPTVPLLLPLVLPALLADVPAGVQGLVPHGDLKRESPPQKQKYNPNSTICT 60  
1 MGLSTVPLLLPLVLLBLVIGIYPSGVGLVPHGLDKRSDVCPQKXIHPONNISICT 60  
61 KCHKGTLYNDPCPGRDTRCVACPTTYALLENHRLRCLSCSRGRDMPFVIEISPCVVD 120  
61 KCHKGTLYNDPCPGRDTRCVACPTTYALLENHRLRCLSCSRGRDMPFVIEISPCVVD 120  
121 RDTVCGCKNOYREYWGTRCLNCSLCFNGTNNI PCOEKODTICHGMGFLKAGACI 180  
121 RDTVCGCKNOYREYWGTRCLNCSLCFNGTNNI PCOEKODTICHGMGFLKAGACI 180  
121 RDTVCGCKNOYREYWGTRCLNCSLCFNGTNNI PCOEKODTICHGMGFLKAGACI 180  
181 SCHDCKNK-ECCKLCPTPSTGKSDODPDTTLLPLVIFGLCLASFASVVLACRYGRMK 239  
181 SCHDCKNK-ECCKLCPTPSTGKSDODPDTTLLPLVIFGLCLASFASVVLACRYGRMK 239  
181 SCHDCKNK-ECCKLCPTPSTGKSDODPDTTLLPLVIFGLCLASFASVVLACRYGRMK 239  
240 PKLYSIICGOSTLYKEGEP-LLVPAGFNP-TTTCFSSTPSSSPVSIIPYI 290  
241 SKLYSIVCGKSTPEKEGELBGTTRKPLAPNPSFPTPGFTPLGFSVPSSSTFTSSYTT 300  
291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350  
301 PGDCPNF---AAPREVAAPYOGADPIL-----ATAL-----ASDPIP 335  
351 TPVQKESASAPADQLADADPATLYAVADGVPSPRWELVRILGSLSEHIERLENGR 410  
336 NPLQKMEISA-HKQSLDTPDPAITYAVENVPLRWKPEFARRGLSHEIDRLQLQNGR 394  
411 HLEAQSMLAAMRRRTPRREATTLELLGRVLRDMDLGCLLENIBALGAARLASEPRL 470  
395 CLREAQYMLATWRRRTPRREATTLELLGRVLRDMDLGCLLENIBALGAARLASEPRL 454

RESULT 13  
US-09-252-656B-3  
Sequence 3, Application US/09252656B  
Patent No. 6495520  
GENERAL INFORMATION:  
APPLICANT: Ebner, Reinhard  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ruben, Steven M.  
APPLICANT: Zhang, Jun  
APPLICANT: Ullrich, Stephen  
APPLICANT: Zhai, Yifan  
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
FILE REFERENCE: 1488.0650006  
CURRENT APPLICATION NUMBER: US/09/252,656B  
PRIOR FILING DATE: 1999-02-19  
PRIOR APPLICATION NUMBER: US 60/075,409  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 09/027,287  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 09/003,886  
PRIOR FILING DATE: 1998-01-07  
PRIOR APPLICATION NUMBER: US 08/822,953  
PRIOR FILING DATE: 1997-03-21  
PRIOR APPLICATION NUMBER: US 60/013,923  
PRIOR FILING DATE: 1996-03-22  
PRIOR APPLICATION NUMBER: US 60/030,157  
PRIOR FILING DATE: 1996-10-31  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-252-656B-3

Query Match 58.3%; Score 1517; DB 4; Length 455;  
Best Local Similarity 62.9%; Pred. No. 1.5e-111;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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QY 1 MGLPTVPGILLPLVLPALLADVPAGVQGLVPHPGDLEKRESPPCGKXNHPONSTICT 60
DB 1 MGLSTVPDLILLPLVLELVGIVPSGVIGLVPHLGRKRDSDVCPQGXIHPONNISICT 60
QY 61 KHKSTVLYNDCPGRGDTDCRVCAPGTYTALBNLRCLSCSRCDMFOVEISPQVVD 120
DB 61 KHKSTVLYNDCPGRGDTDCRVCAPGTYTALBNLRCLSCSRCDMFOVEISPQVVD 120
QY 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCQERODTICHCHMGFFLGAKCI 180
DB 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCQERODTICHCHMGFFLGAKCI 180
QY 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCQERODTICHCHMGFFLGAKCI 180
DB 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCQERODTICHCHMGFFLGAKCI 180
QY 181 SCHDCKK-EECKLCPTRPSTGKSDODPGTTLVLPVIVFGICLASFASVVLACYQKWK 239
DB 181 SCHDCKK-EECKLCPTRPSTGKSDODPGTTLVLPVIVFGICLASFASVVLACYQKWK 239
QY 240 PLYVSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICSPSPSSPVSIPIYI 290
DB 240 PLYVSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICSPSPSSPVSIPIYI 290
QY 241 SKLVSIYCGKSTPEKEGLEGTTRKPLAPNPSFSPTPGFTPLGFSVPVPSSTFTSSSTYT 300
DB 241 SKLVSIYCGKSTPEKEGLEGTTRKPLAPNPSFSPTPGFTPLGFSVPVPSSTFTSSSTYT 300
QY 291 SCDRNFCAVAVSPSSETAPPHLKAGPIILPGPPASTHLCTPGPASTHLCTPGPASTHLCT 350
DB 291 SCDRNFCAVAVSPSSETAPPHLKAGPIILPGPPASTHLCTPGPASTHLCTPGPASTHLCT 350
QY 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPIIP 335
DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPIIP 335
QY 351 TPVQKWEASAPADQADADPATLYAVVDGVPSPRKEVLVRGLSHEIERLEENGR 410
DB 351 TPVQKWEASAPADQADADPATLYAVVDGVPSPRKEVLVRGLSHEIERLEENGR 410
QY 336 NPLQKWEASA-HKPSLDTDPRTLYAVVENVPPLRMEFVRRLGISHEIDRLQLONGR 394
DB 336 NPLQKWEASA-HKPSLDTDPRTLYAVVENVPPLRMEFVRRLGISHEIDRLQLONGR 394
QY 411 HLEAQSMLAAMRRRTPRREATELLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 470
DB 411 HLEAQSMLAAMRRRTPRREATELLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 470
QY 395 CLREAOYSMLATWRRTRRREATELLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 454
DB 395 CLREAOYSMLATWRRTRRREATELLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 454

```

RESULT 14  
US-08-050-319B-25  
Sequence 25, Application US/08050319B  
Patent No. 5633145

GENERAL INFORMATION:  
APPLICANT: M. Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M. Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robbings  
STREET: 635 Bryant Street,  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050.319B  
FILING DATE: 10-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbings, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-050-319B-25

Query Match 58.1%; Score 1512; DB 1; Length 455;  
Best Local Similarity 62.7%; Pred. No. 3,6e-111;  
Matches 301; Conservative 38; Mismatches 109; Indels 36; Gaps 7;

```

QY 1 MGLPTVPGILLPLVLPALLADVPAGVQGLVPHPGDLEKRESPPCGKXNHPONSTICT 60
DB 1 MGLSTVPDLILLPLVLELVGIVPSGVIGLVPHLGRKRDSDVCPQGXIHPONNISICT 60
QY 61 KHKSTVLYNDCPGRGDTDCRVCAPGTYTALBNLRCLSCSRCDMFOVEISPQVVD 120
DB 61 KHKSTVLYNDCPGRGDTDCRVCAPGTYTALBNLRCLSCSRCDMFOVEISPQVVD 120
QY 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCQERODTICHCHMGFFLGAKCI 180
DB 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCQERODTICHCHMGFFLGAKCI 180
QY 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCQERODTICHCHMGFFLGAKCI 180
DB 121 RDTVCGCRKNQYREYMGTFGRCLNCSLCPNGTVNI PCQERODTICHCHMGFFLGAKCI 180
QY 181 SCHDCKK-EECKLCPTRPSTGKSDODPGTTLVLPVIVFGICLASFASVVLACYQKWK 239
DB 181 SCHDCKK-EECKLCPTRPSTGKSDODPGTTLVLPVIVFGICLASFASVVLACYQKWK 239
QY 240 PLYVSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICSPSPSSPVSIPIYI 290
DB 240 PLYVSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICSPSPSSPVSIPIYI 290
QY 241 SKLVSIYCGKSTPEKEGLEGTTRKPLAPNPSFSPTPGFTPLGFSVPVPSSTFTSSSTYT 300
DB 241 SKLVSIYCGKSTPEKEGLEGTTRKPLAPNPSFSPTPGFTPLGFSVPVPSSTFTSSSTYT 300
QY 291 SCDRNFCAVAVSPSSETAPPHLKAGPIILPGPPASTHLCTPGPASTHLCTPGPASTHLCT 350
DB 291 SCDRNFCAVAVSPSSETAPPHLKAGPIILPGPPASTHLCTPGPASTHLCTPGPASTHLCT 350
QY 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPIIP 335
DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATAL-----ASDPIIP 335
QY 351 TPVQKWEASAPADQADADPATLYAVVDGVPSPRKEVLVRGLSHEIERLEENGR 410
DB 351 TPVQKWEASAPADQADADPATLYAVVDGVPSPRKEVLVRGLSHEIERLEENGR 410
QY 336 NPLQKWEASA-HKPSLDTDPRTLYAVVENVPPLRMEFVRRLGISHEIDRLQLONGR 394
DB 336 NPLQKWEASA-HKPSLDTDPRTLYAVVENVPPLRMEFVRRLGISHEIDRLQLONGR 394
QY 411 HLEAQSMLAAMRRRTPRREATELLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 470
DB 411 HLEAQSMLAAMRRRTPRREATELLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 470
QY 395 CLREAOYSMLATWRRTRRREATELLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 454
DB 395 CLREAOYSMLATWRRTRRREATELLELGRVLRDMDLGLCLENIEBALGGAARLASEPRL 454

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RESULT 15  
US-08-465-982-25  
Sequence 25, Application US/08465982  
Patent No. 5863786

GENERAL INFORMATION:  
APPLICANT: M. Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M. Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robbings  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465.982  
FILING DATE: 10-May-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/050.319  
FILING DATE: 10-May-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbings, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-465-982-25

Query Match 58.1%; Score 1512; DB 2; Length 455;  
Best Local Similarity 62.7%; Pred. No. 3,6e-111;

Matches 301; Conservative 38; Mismatches 105; Indels 36; Gaps 7;

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QY 1 MGLEPTVPCGLLPLVLPALADVPAGVQGLVPHRGDLEKRESPPCGKYNHNPONSTICCT 60
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DB 1 MGLETPDILLPLVLLBLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPONNSICCT 60
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QY 61 KCHKGTLYNDCCPGGRDTCRCVCAPGTYTALLENHRLRCLSCSRCDMEFQVEIISPCVVD 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 KCHKGTLYNDCCPGGDTCRCCESSGFTASENHLRHCLSCSKCKEMGQVEISSCTVD 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 RDTVCGCRKQYRYEYWGEGTGFCLNCSICPNGVTNIPQERODTICCHMGFFLKAKCI 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 RDTVCGCRKQYRYHWSENLFCFCNCSICLNGTVHLSCQEKQNTVCTCHAGFFLENECV 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 181 SCHDCKRK-EEKLCPTRRPSTGKDSODPGTVALPIVIVFGLCLASFASVYLACRYORMK 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 SCNNCKKSLBECTKLCLEIENNVKGTEDSGTVLLPLVLPGLCLSLFLGLMTRYORMK 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 240 PKLYSIICGOSTLVKEGEPE-----LVPAPGPNP---TTICFSSSTPSSSPVSIPIPYI 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 SKLYSIYCGKSTPEKEGELBETTKPLAPNPSFSGPTPLGSPVPSSTFTSSSTYT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 291 SCDSNFGAVASPSSETAPPHLKAGPIILGPPASTHLCTGPPASTHLCTGPPASTHLCTC 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 PGDCPNF---AAPREVAPYQADPIL-----ATAL-----ASDPIP 335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 351 TPVQKWEASAPADQADADPATLYAVVDGVPSPRKEIVRIGLSEHETLELLENGR 410
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 336 NPLQKWEUSA-HKQSLDTPDPRITLYAVENVPLRMKEFVRRGLSDHEIDRLQLONGR 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 411 HLRBAQYSMLAAMRRTPRRBATLELGRVLRDMDLGLCLNIEBALGAARLASERPRL 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 395 CLRBAQYMLATWRRTRRBATLELGRVLRDMDLGLCLNIEBALGPAALPPAPSL 454
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Search completed: September 13, 2003, 07:06:40  
Job time : 23 sec

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2003, 07:05:40 ; Search time 26 Seconds

(without alignments)  
2643.260 Million cell updates/sec

Title: US-09-970-532-2

Perfect score: 2603 1 MGLPTVPGLLPLVLPALLA.....NIEBALGGAARLASEPRILW 471

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 6: /cgn2\_6/ptodata/2/pubpaa/PCTIS\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	2603	100.0	471	9	US-09-970-532-2
2	1519	58.4	455	15	US-10-252-408-4
3	1517	58.3	455	9	US-09-826-212-3
4	1517	58.3	455	9	US-09-333-966-5
5	1517	58.3	455	9	US-09-027-287-3
6	1517	58.3	455	9	US-09-874-138-3
7	1517	58.3	455	9	US-09-840-707A-16
8	1517	58.3	455	9	US-09-252-656B-3
9	1517	58.3	455	9	US-09-899-422-2
10	1517	58.3	455	10	US-09-935-727-17
11	1517	58.3	455	10	US-09-898-234-2
12	1517	58.3	455	10	US-09-898-234-17
13	1517	58.3	455	10	US-09-756-854-5
14	1517	58.3	455	10	US-09-899-429A-2
15	1517	58.3	455	10	US-09-899-429A-2

16	1517	58.3	455	10	US-09-899-429A-27	Sequence 27, Appl
17	1517	58.3	455	10	US-09-792-356-2	Sequence 2, Appl
18	1517	58.3	455	10	US-09-792-356-17	Sequence 17, Appl
19	1517	58.3	455	11	US-09-314-889-5	Sequence 5, Appl
20	1517	58.3	455	13	US-10-005-842-3	Sequence 3, Appl
21	1517	58.3	455	14	US-10-120-397-2	Sequence 2, Appl
22	1517	58.3	455	15	US-10-041-574-5	Sequence 5, Appl
23	1517	58.3	455	15	US-10-038-557A-16	Sequence 16, Appl
24	1517	58.3	455	15	US-10-175-902-4	Sequence 4, Appl
25	1517	58.3	455	15	US-10-186-643-3	Sequence 3, Appl
26	1511	58.0	455	12	US-09-899-422-15	Sequence 12, Appl
27	1500.5	57.6	909	15	US-10-226-296-4	Sequence 4, Appl
28	1500.5	57.6	909	15	US-10-226-318-4	Sequence 4, Appl
29	1325.5	50.9	461	9	US-09-899-422-15	Sequence 15, Appl
30	1325.5	50.9	461	10	US-09-898-234-15	Sequence 15, Appl
31	1325.5	50.9	461	10	US-09-899-429A-25	Sequence 25, Appl
32	1325.5	50.9	461	10	US-09-792-356-15	Sequence 15, Appl
33	1178	45.3	371	9	US-09-899-422-12	Sequence 12, Appl
34	1178	45.3	371	10	US-09-898-234-12	Sequence 12, Appl
35	1178	45.3	371	10	US-09-792-356-12	Sequence 12, Appl
36	1171	45.0	371	10	US-09-899-429A-22	Sequence 22, Appl
37	1072	41.2	247	9	US-09-970-532-4	Sequence 4, Appl
38	874	33.6	213	15	US-10-193-616-10	Sequence 10, Appl
39	834.5	32.1	213	14	US-10-125-062-1	Sequence 1, Appl
40	832.5	32.0	211	10	US-09-899-429A-8	Sequence 8, Appl
41	813.5	31.3	197	14	US-10-112-793-21	Sequence 21, Appl
42	813.5	31.3	201	10	US-09-899-429A-14	Sequence 14, Appl
43	772	29.7	200	10	US-09-899-429A-12	Sequence 12, Appl
44	753	28.9	190	10	US-09-899-429A-18	Sequence 18, Appl
45	738.5	28.4	183	10	US-09-899-429A-10	Sequence 10, Appl

#### ALIGNMENTS

RESULT 1

US-09-970-532-2

Sequence 2, Application US/09970532

Patent No. US20020076765A1

GENERAL INFORMATION:

APPLICANT: Taylor, J. Michael

APPLICANT: Kenrill, J.F., Marcus

APPLICANT: Lee, Sun-Kyung

APPLICANT: Mwang, Simon

TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1

TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: 06411-018001

CURRENT FILING DATE: 2001-10-03

CURRENT APPLICATION NUMBER: US/09/970,532

PRIOR FILING DATE: 09/513,007

PRIOR APPLICATION NUMBER: 2000-02-25

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 471

TYPE: PRT

ORGANISM: Bos taurus

US-09-970-532-2

Query Match 100.0%; Score 2603; DB 9; Length 471;

Best Local Similarity 100.0%; Pred. No. 1.1e-178;

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLPTVPGLLPLVLPALLADYVAGVGVLPHPGDLKRESPOCGKYNPNOSTICT 60

DB 1 MGLPTVPGLLPLVLPALLADYVAGVGVLPHPGDLKRESPOCGKYNPNOSTICT 60

QY KCHGTYLYNDPCPGGRDTCVCAPGTYTALBNHLRCLSCSRCDMPVBSICVVD 120

DB KCHGTYLYNDPCPGGRDTCVCAPGTYTALBNHLRCLSCSRCDMPVBSICVVD 120

QY 121 RDTVCGKKNQYREYWGRTGRCLNCSICPVGTYNIPQEQDPTTCHGKMFPLKAGNCI 180

DB RDTVCGKKNQYREYWGRTGRCLNCSICPVGTYNIPQEQDPTTCHGKMFPLKAGNCI 180

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Db      121 RDTVCGCRKNQYREYWGTFGRCLNCSLCPNGTIVNI PCQERODTICHGMGFLKAGACI 180
Qy      101 SCHDCKNKECEKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCLASASVLA CRQWRMP 240
Db      101 SCHDCKNKECEKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCLASASVLA CRQWRMP 240
Qy      241 KLYSIICGOSTLVKEGEPELVAPAGFNFTTTCISSTPSSSPVSIPIYISCDRSNFGAV 300
Db      241 KLYSIICGOSTLVKEGEPELVAPAGFNFTTTCISSTPSSSPVSIPIYISCDRSNFGAV 300
Qy      301 ASPSETAPPHLKAGPILPGPPASTHLCCTPGPPASTHLCCTPGPPASTHLCCTPGQKWEASA 360
Db      301 ASPSETAPPHLKAGPILPGPPASTHLCCTPGPPASTHLCCTPGPPASTHLCCTPGQKWEASA 360
Qy      361 PSAPQOLADADPATLYAAVDGVPPSRWKELVRLGLSEHEIERLEENGRHIREAOYSML 420
Db      361 PSAPQOLADADPATLYAAVDGVPPSRWKELVRLGLSEHEIERLEENGRHIREAOYSML 420
Qy      421 AAMRRRTTREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLLM 471
Db      421 AAMRRRTTREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLLM 471

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## RESULT 2

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US-10-252-408-4
/ Sequence 4, Application US/10252408
/ Publication No. US20030082736A1
/ GENERAL INFORMATION:
/ APPLICANT: SMITH, Craig A.
/ TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
/ FILE REFERENCE: A-71592
/ CURRENT APPLICATION NUMBER: US/10/252,408
/ PRIOR FILING DATE: 2002-09-24
/ PRIOR APPLICATION NUMBER: US/08/406,824
/ PRIOR FILING DATE: 1995-03-20
/ PRIOR APPLICATION NUMBER: US 08/255,849
/ PRIOR FILING DATE: 1994-06-08
/ PRIOR APPLICATION NUMBER: US 07/860,710
/ PRIOR FILING DATE: 1992-03-30
/ PRIOR APPLICATION NUMBER: US 07/523,635
/ PRIOR FILING DATE: 1990-05-10
/ PRIOR APPLICATION NUMBER: US 07/421,417
/ PRIOR FILING DATE: 1989-10-13
/ PRIOR APPLICATION NUMBER: US 07/405,370
/ PRIOR FILING DATE: 1989-09-11
/ PRIOR APPLICATION NUMBER: US 07/403,241
/ PRIOR FILING DATE: 1989-09-05
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 4
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-252-408-4

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Query Match 58.4%; Score 1519; DB 15; Length 455;

Best Local Similarity 62.9%; Pred. No. 5,1e-101;

Matches 302; Conservative 39; Mismatches 103; Indels 36; Gaps 7;

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Qy      1 MGLPTVPGLLLPLVLPALLADYYPAGVOGLVPHPDLEKRESPPCQKGYNHPONSTICT 60
Db      1 MGLSTVPDLLPLVLLELVGIVPSGVIGLVPHLDREKRDSVCPQKGYIHPONNSICT 60
Qy      61 KCHKGTLYVNDPCPGGRDTCRCVCAFGTYTALLENHLRCLSCSRDDEMFOVEISPCYVD 120
Db      61 KCHKGTLYVNDPCPGGRDTCRCVCAFGTYTALLENHLRCLSCSRDDEMFOVEISPCYVD 120
Qy      121 RDTVCGCRKNQYREYWGTFGRCLNCSLCPNGTIVNI PCQERODTICHGMGFLKAGACI 180
Db      121 RDTVCGCRKNQYREYWGTFGRCLNCSLCPNGTIVNI PCQERODTICHGMGFLKAGACI 180
Qy      181 SCHDCKN-EEBKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCLASASVLA CRQWRMP 239
Db      181 SCHDCKN-EEBKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCLASASVLA CRQWRMP 239

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Db      181 SCNNCKSLBECTKCLCPQIENWKTGDSGTTVLLPLVIVFGLCLSLFLIGLSYNRQWK 240
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Db      241 SKLYSIIVGKSTPEKEGELBEGTTTKPLAPNPSFSPTPGFTPLGSPVPSSTFTSSSTYT 300
Qy      291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCCTPGPPASTHLCCTPGPPASTHLC 350
Db      301 PDCPCNF---AAPREVAPPYOGADPIL-----ATL-----ASDP 335
Qy      351 TPVQKWEASAPADQOLADADPATLYAAVDGVPPSRWKELVRLGLSEHEIERLEENGR 410
Db      336 NPLQKWEBSA-HKPOSIDTDADPATLYAAVENVPPLRWKEFVRRLGSLDHEIDRLQNGR 394
Qy      411 HIREAOYSMLAAMRRRTTREATLELLGRVLRDMDLGCLENIEEALGGAARLASEPRLL 470
Db      395 CLREAOYSMLAAMRRRTTREATLELLGRVLRDMDLGCLDIEBALGPAALPPAPSL 454

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## RESULT 3

```

US-09-826-212-3
/ Sequence 3, Application US/09826212
/ Patent No. US20010021516A1
/ GENERAL INFORMATION:
/ APPLICANT: Wei, Ying-Fei
/ APPLICANT: Gentz, Reinex
/ APPLICANT: Ruben, Steven
/ APPLICANT: Ni, Jian
/ TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
/ FILE REFERENCE: 1488,1280006
/ CURRENT APPLICATION NUMBER: US/09/826,212
/ PRIOR FILING DATE: 2001-04-05
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: Patent version 3.0
/ SEQ ID NO 3
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-826-212-3

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Query Match 58.3%; Score 1517; DB 9; Length 455;

Best Local Similarity 62.9%; Pred. No. 7,1e-101;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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Qy      1 MGLPTVPGLLLPLVLPALLADYYPAGVOGLVPHPDLEKRESPPCQKGYNHPONSTICT 60
Db      1 MGLSTVPDLLPLVLLELVGIVPSGVIGLVPHLDREKRDSVCPQKGYIHPONNSICT 60
Qy      61 KCHKGTLYVNDPCPGGRDTCRCVCAFGTYTALLENHLRCLSCSRDDEMFOVEISPCYVD 120
Db      61 KCHKGTLYVNDPCPGGRDTCRCVCAFGTYTALLENHLRCLSCSRDDEMFOVEISPCYVD 120
Qy      121 RDTVCGCRKNQYREYWGTFGRCLNCSLCPNGTIVNI PCQERODTICHGMGFLKAGACI 180
Db      121 RDTVCGCRKNQYREYWGTFGRCLNCSLCPNGTIVNI PCQERODTICHGMGFLKAGACI 180
Qy      181 SCHDCKN-EEBKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCLASASVLA CRQWRMP 239
Db      181 SCHDCKN-EEBKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCLASASVLA CRQWRMP 239
Qy      240 PKLYSIICGOSTLVKEGEPE-----LVVAPAGFN-----TTTICSSSTPSSSPVSIPIYI 290
Db      241 SKLYSIIVGKSTPEKEGELBEGTTTKPLAPNPSFSPTPGFTPLGSPVPSSTFTSSSTYT 300
Qy      291 SCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCCTPGPPASTHLCCTPGPPASTHLC 350
Db      301 PGDCPNF---AAPREVAPPYOGADPIL-----ATL-----ASDP 335
Qy      351 TPVQKWEASAPADQOLADADPATLYAAVDGVPPSRWKELVRLGLSEHEIERLEENGR 410
Db      336 NPLQKWEBSA-HKPOSIDTDADPATLYAAVENVPPLRWKEFVRRLGSLDHEIDRLQNGR 394
Qy      411 HIREAOYSMLAAMRRRTTREATLELLGRVLRDMDLGCLDIEBALGPAALPPAPSL 470

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Db 395 CLREAQYSMLATWRRRTFRREATTLELLGRVLRDMDLLGCLIEDIBALCGPALPPAPSL 454

# RESULT 4

US-09-333-966-5

Sequence 5, Application US/09333966

Patent No. US20020009773A1

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang

APPLICANT: Ni, Jian

APPLICANT: Dixit, Vishva

APPLICANT: Gentz, Reiner L.

APPLICANT: Dillon, Patrick J.

TITLE OF INVENTION: Death Domain Containing Receptors

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., NW, Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/333, 966

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/815, 469

FILING DATE:

APPLICATION NUMBER: No. US20020009773A1 Yet Assigned

FILING DATE: 06-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/028, 711

FILING DATE: 17-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/013, 285

FILING DATE: 12-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36, 688

REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 455 amino acids

TYPE: amino acid

STRANDEDNESS: No. US20020009773A1 Relevant

TOPOLOGY: No. US20020009773A1 Relevant

MOLECULE TYPE: protein

US-09-333-966-5

# Query Match

Best Local Similarity 58.3%; Score 1517; DB 9; Length 455;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

1 MGLPTVPLLLPLVLPALLADVYPAGVQGLVPHPDLEKRESPPQGGKYNNPONSITCT 60

1 MGLSTVPLLLPLVLELVGITYSGVIGLVPHLDREKRSVCPQGGKIHPONNSICT 60

1 MGLSTVPLLLPLVLELVGITYSGVIGLVPHLDREKRSVCPQGGKIHPONNSICT 60

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

Db 121 RDTVCGCKRNOYREWGRTGRCLNCSLCPNGTNNIPQERODTICHGMGFFLGKACI 180

Db 181 SCHDCKNK-ECEKLCPTRPSTGKDSODPGTTLVLPVIFGLCLASFASVVLACRYGRMK 239

Db 181 SCNNCKSLECKTCLPQIENVKGTBDGSGTTLVLPVIFGLCLSLFLGLMRYGRMK 240

Db 240 PKLYSIICGOSTLYKEGEP-----LVPAPGNP-----TTTICRSSTPSSSPVSIPIYI 290

Db 241 SKLYSIICGOSTLYKEGEP-----LVPAPGNP-----TTTICRSSTPSSSPVSIPIYI 300

Db 291 SCDSNPGAVASPESEAPPHLXAGPILPGPASTHCTPSPASTHCTGPPASTHCTC 350

Db 301 PGDCPNF---AAPRRVAPPYQADPIL-----ATAL-----ASDIP 335

Db 351 TPVCKEASAPADOLADADPATLYAVVDGVPSPRWKELVRLGLSHEIRLENGR 410

Db 336 NPLOKMBESA-HKQSLDTDDPATLYAVVEVPLPAPWEPFRRGLSHEIRLENGR 394

Db 411 HLEDAQYSMLATWRRRTFRREATTLELLGRVLRDMDLLGCLIEDIBALCGPALPPAPSL 470

Db 395 CLREAQYSMLATWRRRTFRREATTLELLGRVLRDMDLLGCLIEDIBALCGPALPPAPSL 454

# RESULT 5

US-09-027-287-3

Sequence 3, Application US/09027287A

Patent No. US20020064869A1

GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard

APPLICANT: Yu, Guo-Liang

APPLICANT: Ruben, Steven M.

APPLICANT: Ullrich, Stephen

TITLE OF INVENTION: Apoptosis Inducing Molecule II

FILE REFERENCE: 1488.0650004

CURRENT APPLICATION NUMBER: US/09/027, 287A

FILING DATE: 1998-02-20

EARLIER APPLICATION NUMBER: US 09/003, 886

EARLIER FILING DATE: 1998-01-07

EARLIER APPLICATION NUMBER: US 60/822, 953

EARLIER FILING DATE: 1997-03-21

EARLIER APPLICATION NUMBER: US 60/030, 157

EARLIER FILING DATE: 1996-10-31

EARLIER APPLICATION NUMBER: US 60/013, 923

EARLIER FILING DATE: 1996-03-22

NUMBER OF SEQ ID NOS: 55

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 455

TYPE: PRT

ORGANISM: Homo sapiens

US-09-027-287-3

# Query Match

Best Local Similarity 58.3%; Score 1517; DB 9; Length 455;

Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

1 MGLPTVPLLLPLVLPALLADVYPAGVQGLVPHPDLEKRESPPQGGKYNNPONSITCT 60

1 MGLSTVPLLLPLVLELVGITYSGVIGLVPHLDREKRSVCPQGGKIHPONNSICT 60

1 MGLSTVPLLLPLVLELVGITYSGVIGLVPHLDREKRSVCPQGGKIHPONNSICT 60

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

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1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

1 KCHGKTYLYNDPCPGGRDTRVCAPGTYYALLENHRLRCLSCSRCDDEMFOVEISPCVVD 120

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Db 241 SKLVSIVCGKSTPEKEGELGTTTKPLAHPSPFSTPGFTTTLGSPVPSSTFTSSSTYT 300
Qy 291 SCDSNFGAVASPSSETPAPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
Db 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
Qy 351 TPVOKMEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRRLGLSEHIERLENGR 410
Db 336 NPLQKMEBSA-HKPSLTDDBPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLONGR 394
Qy 411 HUREAOYSLAAMRRRTPREATLELLGRVLRDMDLGLCLENIEBALGGAARLASERPUL 470
Db 395 CLREAQYSLATWRRRTPREATLELLGRVLRDMDLGLCLEDIEBALGGAALPPAPSL 454

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RESULT 6  
US-09-874-138-3

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; Sequence 3, Application US/09874138
; Patent No. US20020072091A1
; GENERAL INFORMATION:
; APPLICANT: N1, Jian
; APPLICANT: Genetz, Reiner L.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.131006
; CURRENT APPLICATION NUMBER: US/09/874.138
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/565.009
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148.939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133.238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132.498
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042.583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054.021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040.846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-874-138-3

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Query Match 58.3%; Score 1517; DB 9; Length 455;

Best Local Similarity 62.9%; Pred. No. 7.1e-101; Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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Qy 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHGDLKRESPPCGKYNHFNPNSTICT 60
Db 1 MGLSTVPDLLPLVLLELVGLVIGVGLVPHGLDREKRSVCGKVIHPNNSICT 60
Qy 61 KCHKTYLYNDPCPGGRDTCRVCAPGTYTLLENHRLRCLSCSRCDMPFQVEISPCVVD 120
Db 61 KCHKTYLYNDPCPGGRDTCRVCAPGTYTLLENHRLRCLSCSRCKEMGVIEISSCTVD 120
Qy 121 RDTVCGCKRNOYREYMGRTGFRCLNCSLCPNGTVINIPCOBRDTHCHGMGFLKAGCI 180
Db 121 RDTVCGCKRNOYRHVMSNLFCGFCNCSLCNCTVHLSCOEKONTVCTCHAGFFLENECV 180
Qy 181 SCHDCCKN-ECEKLCPTRPSTGKSDODPGTTVLLPLVIVFGICLASFASVVLACRYORMK 239
Db 181 SCNSCKSLKCTKCLPQIEHVKGTEBGGTTVLLPLVIFGICLSLFLIGLMRYQRMK 240
Qy 240 PKLYSIIGOSTLVKESGPE-----LVVAPAGFNP-----TTTICSSSTPSSSPVSIPIYI 290
Db 240 PKLYSIIGOSTLVKESGPE-----LVVAPAGFNP-----TTTICSSSTPSSSPVSIPIYI 290

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Db 241 SKLVSIVCGKSTPEKEGELGTTTKPLAHPSPFSTPGFTTTLGSPVPSSTFTSSSTYT 300
Qy 291 SCDSNFGAVASPSSETPAPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
Db 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
Qy 351 TPVOKMEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRRLGLSEHIERLENGR 410
Db 336 NPLQKMEBSA-HKPSLTDDBPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLONGR 394
Qy 411 HUREAOYSLAAMRRRTPREATLELLGRVLRDMDLGLCLENIEBALGGAARLASERPUL 470
Db 395 CLREAQYSLATWRRRTPREATLELLGRVLRDMDLGLCLEDIEBALGGAALPPAPSL 454

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RESULT 7  
US-09-840-707A-16

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; Sequence 16, Application US/09840707A
; Patent No. US2002007276A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; FILE REFERENCE: 24881-301C
; CURRENT APPLICATION NUMBER: US/09/840.707A
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562.979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198.210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Tumor Necrosis Factor p55 Receptor
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAA36753/GenBank
; DATABASE ENTRY DATE: 1995-08-03
; US-09-840-707A-16

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Query Match 58.3%; Score 1517; DB 9; Length 455;

Best Local Similarity 62.9%; Pred. No. 7.1e-101; Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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Qy 1 MGLPTVPGLLPLVLPALLADVPAGVGLVPHGDLKRESPPCGKYNHFNPNSTICT 60
Db 1 MGLSTVPDLLPLVLLELVGLVIGVGLVPHGLDREKRSVCGKVIHPNNSICT 60
Qy 61 KCHKTYLYNDPCPGGRDTCRVCAPGTYTLLENHRLRCLSCSRCDMPFQVEISPCVVD 120
Db 61 KCHKTYLYNDPCPGGRDTCRVCAPGTYTLLENHRLRCLSCSRCKEMGVIEISSCTVD 120
Qy 121 RDTVCGCKRNOYREYMGRTGFRCLNCSLCPNGTVINIPCOBRDTHCHGMGFLKAGCI 180
Db 121 RDTVCGCKRNOYRHVMSNLFCGFCNCSLCNCTVHLSCOEKONTVCTCHAGFFLENECV 180
Qy 181 SCHDCCKN-ECEKLCPTRPSTGKSDODPGTTVLLPLVIVFGICLASFASVVLACRYORMK 239
Db 181 SCNSCKSLKCTKCLPQIEHVKGTEBGGTTVLLPLVIFGICLSLFLIGLMRYQRMK 240
Qy 240 PKLYSIIGOSTLVKESGPE-----LVVAPAGFNP-----TTTICSSSTPSSSPVSIPIYI 290
Db 241 SKLVSIVCGKSTPEKEGELGTTTKPLAHPSPFSTPGFTTTLGSPVPSSTFTSSSTYT 300
Qy 291 SCDSNFGAVASPSSETPAPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
Db 301 PGDCPNF---AAPREVAPPYOGADPIL-----ATAL-----ASDPIP 335
Qy 351 TPVOKMEASAPAPQDLADADPATLYAVVDGVPSPRWKELVRRLGLSEHIERLENGR 410

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Db 336 NPLQKWEBSA-HKQSLDTPDPAVLAVENVPLRWEKFRRLGLSDHEIDRLQNGR 394  
 Oy 411 HLEAAYSMIAAMRRTPREATLELGRVLRDMDLGCLENIEEALGAARLASERPLL 470  
 Db 395 CLREAQYSMLATWRKTRPREATLELGRVLRDMDLGCLEDIEBALCGPALPPASLL 454

## RESULT 8

US-09-252-656B-3  
 ; Sequence 3, Application US/09252656B  
 ; Patent No. US20020081647A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ebner, Reinhard  
 ; APPLICANT: Yu, Guo-liang  
 ; APPLICANT: Ruben, Steven M.  
 ; APPLICANT: Zhang, Jun  
 ; APPLICANT: Ullrich, Stephen  
 ; APPLICANT: Zhai, Yifan  
 ; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
 ; FILE REFERENCE: 1488.065006  
 ; CURRENT APPLICATION NUMBER: US/09/252,656B  
 ; PRIOR FILING DATE: 1999-02-19  
 ; PRIOR APPLICATION NUMBER: US 60/075,409  
 ; PRIOR FILING DATE: 1998-02-20  
 ; PRIOR APPLICATION NUMBER: US 09/027,287  
 ; PRIOR FILING DATE: 1998-02-20  
 ; PRIOR APPLICATION NUMBER: US 09/003,886  
 ; PRIOR FILING DATE: 1998-01-07  
 ; PRIOR APPLICATION NUMBER: US 08/822,953  
 ; PRIOR FILING DATE: 1997-03-21  
 ; PRIOR APPLICATION NUMBER: US 60/013,923  
 ; PRIOR FILING DATE: 1996-03-22  
 ; PRIOR APPLICATION NUMBER: US 60/030,157  
 ; PRIOR FILING DATE: 1996-10-31  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 455  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-252-656B-3

Query Match 58.3%; Score 1517; DB 9; Length 455;  
 Best Local Similarity 62.9%; Pred. No. 7,1e-101;  
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Oy 1 MGLPTVPLLLPLVLPALLADYYPAGVGLVPHPDLEKRESPPCQGRKNHPONSTICT 60  
 Db 1 MGLSTVPDLLPLVLLELVGIVPSGVIGLVPHLGDREKRDVSCPOGRKXIHPONNISICT 60  
 Oy 61 KCHGKTYLYNDCCPGGRDTCRCVCAFGTYTLEHNLARCLSCSRCDMPFOVEISPCVVD 120  
 Db 61 KCHKGTLYLNDCCPGGRDTCRCVCAFGTYTLEHNLARCLSCSRCDMPFOVEISPCVVD 120  
 Oy 121 RDTVCGCKNORYRHWGRTGFRCLNCSLCPNGTVNIPCOERODTICHGMFPLKAGACI 180  
 Db 121 RDTVCGCKNORYRHWGRTGFRCLNCSLCPNGTVNIPCOERODTICHGMFPLKAGACI 180  
 Oy 121 RDTVCGCKNORYRHWGRTGFRCLNCSLCPNGTVNIPCOERODTICHGMFPLKAGACI 180  
 Db 121 RDTVCGCKNORYRHWGRTGFRCLNCSLCPNGTVNIPCOERODTICHGMFPLKAGACI 180  
 Oy 181 SCHDCKNK-EECKLCPTRPSTGKSDODPGTTLPLVLVIFGLCLASFAVYLACRYGRWK 239  
 Db 181 SCHDCKNK-EECKLCPTRPSTGKSDODPGTTLPLVLVIFGLCLASFAVYLACRYGRWK 239  
 Oy 181 SCHDCKNK-EECKLCPTRPSTGKSDODPGTTLPLVLVIFGLCLASFAVYLACRYGRWK 239  
 Db 181 SCHDCKNK-EECKLCPTRPSTGKSDODPGTTLPLVLVIFGLCLASFAVYLACRYGRWK 239  
 Oy 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICPSSPSSSPVSIPIYI 290  
 Db 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICPSSPSSSPVSIPIYI 290  
 Oy 241 SKLYSIIVGKSTPEKEGLEGTTRKPLAPNPSFSPGFTPLGSSPVSSSTFTSSSTYT 300  
 Db 241 SKLYSIIVGKSTPEKEGLEGTTRKPLAPNPSFSPGFTPLGSSPVSSSTFTSSSTYT 300  
 Oy 291 SCDSNFGAVASPSETAPPHLKAGPILGPPASTHLCTGPPASTHLCTGPPASTHLCTC 350  
 Db 291 SCDSNFGAVASPSETAPPHLKAGPILGPPASTHLCTGPPASTHLCTGPPASTHLCTC 350  
 Oy 301 PGDCNPF---AAPREVAPPYOGADPIL-----ATL-----ASDPIP 335  
 Db 301 PGDCNPF---AAPREVAPPYOGADPIL-----ATL-----ASDPIP 335  
 Oy 351 TPVQKWEASAPADQDLADADPATLYAVVDGVPSPRWEKLVRLGLSHEIERLENGR 410  
 Db 351 TPVQKWEASAPADQDLADADPATLYAVVDGVPSPRWEKLVRLGLSHEIERLENGR 410

Db 336 NPLQKWEBSA-HKQSLDTPDPAVLAVENVPLRWEKFRRLGLSDHEIDRLQNGR 394  
 Oy 411 HLEAAYSMIAAMRRTPREATLELGRVLRDMDLGCLENIEEALGAARLASERPLL 470  
 Db 395 CLREAQYSMLATWRKTRPREATLELGRVLRDMDLGCLEDIEBALCGPALPPASLL 454

## RESULT 9

US-09-899-422-2  
 ; Sequence 2, Application US/09899422  
 ; Patent No. US20020090676A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hauptmann, Rudolph  
 ; APPLICANT: Hamlet, Adolph  
 ; APPLICANT: Maurer-Fogy, Ingrid  
 ; APPLICANT: Strawowa, Christian  
 ; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
 ; TITLE OF INVENTION: Them  
 ; FILE REFERENCE: 98,385-H  
 ; CURRENT APPLICATION NUMBER: US/09/899,422  
 ; PRIOR FILING DATE: 2001-08-21  
 ; PRIOR APPLICATION NUMBER: 09/525,998  
 ; PRIOR FILING DATE: 2000-03-15  
 ; PRIOR APPLICATION NUMBER: 08/383,676  
 ; PRIOR FILING DATE: 1995-02-01  
 ; PRIOR APPLICATION NUMBER: 08/153,287  
 ; PRIOR FILING DATE: 1993-11-17  
 ; PRIOR APPLICATION NUMBER: 07/821,750  
 ; PRIOR FILING DATE: 1992-01-02  
 ; PRIOR APPLICATION NUMBER: 07/511,430  
 ; PRIOR FILING DATE: 1990-04-20  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 455  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-899-422-2

Query Match 58.3%; Score 1517; DB 9; Length 455;  
 Best Local Similarity 62.9%; Pred. No. 7,1e-101;  
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Oy 1 MGLPTVPLLLPLVLPALLADYYPAGVGLVPHPDLEKRESPPCQGRKNHPONSTICT 60  
 Db 1 MGLSTVPDLLPLVLLELVGIVPSGVIGLVPHLGDREKRDVSCPOGRKXIHPONNISICT 60  
 Oy 61 KCHGKTYLYNDCCPGGRDTCRCVCAFGTYTLEHNLARCLSCSRCDMPFOVEISPCVVD 120  
 Db 61 KCHKGTLYLNDCCPGGRDTCRCVCAFGTYTLEHNLARCLSCSRCDMPFOVEISPCVVD 120  
 Oy 121 RDTVCGCKNORYRHWGRTGFRCLNCSLCPNGTVNIPCOERODTICHGMFPLKAGACI 180  
 Db 121 RDTVCGCKNORYRHWGRTGFRCLNCSLCPNGTVNIPCOERODTICHGMFPLKAGACI 180  
 Oy 121 RDTVCGCKNORYRHWGRTGFRCLNCSLCPNGTVNIPCOERODTICHGMFPLKAGACI 180  
 Db 121 RDTVCGCKNORYRHWGRTGFRCLNCSLCPNGTVNIPCOERODTICHGMFPLKAGACI 180  
 Oy 181 SCHDCKNK-EECKLCPTRPSTGKSDODPGTTLPLVLVIFGLCLASFAVYLACRYGRWK 239  
 Db 181 SCHDCKNK-EECKLCPTRPSTGKSDODPGTTLPLVLVIFGLCLASFAVYLACRYGRWK 239  
 Oy 181 SCHDCKNK-EECKLCPTRPSTGKSDODPGTTLPLVLVIFGLCLASFAVYLACRYGRWK 239  
 Db 181 SCHDCKNK-EECKLCPTRPSTGKSDODPGTTLPLVLVIFGLCLASFAVYLACRYGRWK 239  
 Oy 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICPSSPSSSPVSIPIYI 290  
 Db 240 PKLYSIIGOSTLVKEGPE-----LVVAPGFNP-----TTTICPSSPSSSPVSIPIYI 290  
 Oy 241 SKLYSIIVGKSTPEKEGLEGTTRKPLAPNPSFSPGFTPLGSSPVSSSTFTSSSTYT 300  
 Db 241 SKLYSIIVGKSTPEKEGLEGTTRKPLAPNPSFSPGFTPLGSSPVSSSTFTSSSTYT 300  
 Oy 291 SCDSNFGAVASPSETAPPHLKAGPILGPPASTHLCTGPPASTHLCTGPPASTHLCTC 350  
 Db 291 SCDSNFGAVASPSETAPPHLKAGPILGPPASTHLCTGPPASTHLCTGPPASTHLCTC 350  
 Oy 301 PGDCNPF---AAPREVAPPYOGADPIL-----ATL-----ASDPIP 335  
 Db 301 PGDCNPF---AAPREVAPPYOGADPIL-----ATL-----ASDPIP 335  
 Oy 351 TPVQKWEASAPADQDLADADPATLYAVVDGVPSPRWEKLVRLGLSHEIERLENGR 410  
 Db 351 TPVQKWEASAPADQDLADADPATLYAVVDGVPSPRWEKLVRLGLSHEIERLENGR 410  
 Oy 411 HLEAAYSMIAAMRRTPREATLELGRVLRDMDLGCLENIEEALGAARLASERPLL 470  
 Db 411 HLEAAYSMIAAMRRTPREATLELGRVLRDMDLGCLENIEEALGAARLASERPLL 470

Db 395 CLREAOYSMLATWRRRTPRREATLELLGRVLRMDMLLGGCUEIEEALCGPALPAPASLL 454

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RESULT 10
US-09-899-422-17
; Sequence 17, Application US/09899422
; Patent No. US20020090676M1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hummer, Adolph
; APPLICANT: Maurer-Fog, Ingrid
; APPLICANT: Stralow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNA Coding for
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
US-09-899-422-17
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Query Match 58.3%; Score 1517; DB 9; Length 455;  
Best Local Similarity 62.9%; Pred. No. 7,1e-101;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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QY 1 MGLPTVPGLLPLVLPALADVYVAGVGLVPHPGDLEKESPCPOGKYNHPONSTICT 60
DB 1 MGLSTVPLDLLPLVLELVIGYISGVIGLVPHLGDREKRDVCPQGXIHPONSICT 60
QY 61 KCHKGTLYNDGPGGPDTCRCVCAFGTYTALLENLRCLSCSRKRDMPQVEISPCVD 120
DB 61 KCHKGTLYNDGPGGPDTCRCVCAFGTYTALLENLRCLSCSRKRDMPQVEISPCVD 120
QY 121 RDTVCGCRKNQRYRWGSETGFRCLNCSLCPNGTNIICOERODTICHGMGFLKGAACI 180
DB 121 RDTVCGCRKNQRYRWGSETGFRCLNCSLCPNGTNIICOERODTICHGMGFLKGAACI 180
QY 121 RDTVCGCRKNQRYRWGSETGFRCLNCSLCPNGTNIICOERODTICHGMGFLKGAACI 180
DB 121 RDTVCGCRKNQRYRWGSETGFRCLNCSLCPNGTNIICOERODTICHGMGFLKGAACI 180
QY 161 SCHDCRKN-ECEKLCPTRPSTGKSDQPGTTVLLPLVIVGCLASFASVVLACRYORWK 239
DB 161 SCHDCRKN-ECEKLCPTRPSTGKSDQPGTTVLLPLVIVGCLASFASVVLACRYORWK 239
QY 181 SCNSCKKSLSECTKCLCPQJENYKGTEDSGTTLPLVIFPGCLLSLFLGLMYRYORWK 240
DB 181 SCNSCKKSLSECTKCLCPQJENYKGTEDSGTTLPLVIFPGCLLSLFLGLMYRYORWK 240
QY 240 PKLYSIICGOSTLVKEGEP-----LLVAPGFNP-----TTTICSSSTPSSPVSIPIYI 290
DB 240 PKLYSIICGOSTLVKEGEP-----LLVAPGFNP-----TTTICSSSTPSSPVSIPIYI 290
QY 241 SKLYSIIVCGKSTPEKEGELGTTTKPLAPNPSFSPPTGFTPLIGFSFVPSSTFTSSSTYT 300
DB 241 SKLYSIIVCGKSTPEKEGELGTTTKPLAPNPSFSPPTGFTPLIGFSFVPSSTFTSSSTYT 300
QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
DB 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
QY 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATL-----ASDPIP 335
DB 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATL-----ASDPIP 335
QY 351 TPVQKWEASAPAPQADADPATLYAVVDGVPSPRWKELVRRIGLSEHEIERLENGR 410
DB 351 TPVQKWEASAPAPQADADPATLYAVVDGVPSPRWKELVRRIGLSEHEIERLENGR 410
QY 411 HLREAOYSMLATWRRRTPRREATLELLGRVLRMDMLLGGCUEIEEALCGPALPAPASLL 470
DB 411 HLREAOYSMLATWRRRTPRREATLELLGRVLRMDMLLGGCUEIEEALCGPALPAPASLL 470
QY 395 CLREAOYSMLATWRRRTPRREATLELLGRVLRMDMLLGGCUEIEEALCGPALPAPASLL 454
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RESULT 11
US-09-935-727-5
; Sequence 5, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PFA54P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/166,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-727-5
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Query Match 58.3%; Score 1517; DB 10; Length 455;  
Best Local Similarity 62.9%; Pred. No. 7,1e-101;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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QY 1 MGLPTVPGLLPLVLPALADVYVAGVGLVPHPGDLEKESPCPOGKYNHPONSTICT 60
DB 1 MGLSTVPLDLLPLVLELVIGYISGVIGLVPHLGDREKRDVCPQGXIHPONSICT 60
QY 61 KCHKGTLYNDGPGGPDTCRCVCAFGTYTALLENLRCLSCSRKRDMPQVEISPCVD 120
DB 61 KCHKGTLYNDGPGGPDTCRCVCAFGTYTALLENLRCLSCSRKRDMPQVEISPCVD 120
QY 121 RDTVCGCRKNQRYRWGSETGFRCLNCSLCPNGTNIICOERODTICHGMGFLKGAACI 180
DB 121 RDTVCGCRKNQRYRWGSETGFRCLNCSLCPNGTNIICOERODTICHGMGFLKGAACI 180
QY 121 RDTVCGCRKNQRYRWGSETGFRCLNCSLCPNGTNIICOERODTICHGMGFLKGAACI 180
DB 121 RDTVCGCRKNQRYRWGSETGFRCLNCSLCPNGTNIICOERODTICHGMGFLKGAACI 180
QY 161 SCHDCRKN-ECEKLCPTRPSTGKSDQPGTTVLLPLVIVGCLASFASVVLACRYORWK 239
DB 161 SCHDCRKN-ECEKLCPTRPSTGKSDQPGTTVLLPLVIVGCLASFASVVLACRYORWK 239
QY 181 SCNSCKKSLSECTKCLCPQJENYKGTEDSGTTLPLVIFPGCLLSLFLGLMYRYORWK 240
DB 181 SCNSCKKSLSECTKCLCPQJENYKGTEDSGTTLPLVIFPGCLLSLFLGLMYRYORWK 240
QY 240 PKLYSIICGOSTLVKEGEP-----LLVAPGFNP-----TTTICSSSTPSSPVSIPIYI 290
DB 240 PKLYSIICGOSTLVKEGEP-----LLVAPGFNP-----TTTICSSSTPSSPVSIPIYI 290
QY 241 SKLYSIIVCGKSTPEKEGELGTTTKPLAPNPSFSPPTGFTPLIGFSFVPSSTFTSSSTYT 300
DB 241 SKLYSIIVCGKSTPEKEGELGTTTKPLAPNPSFSPPTGFTPLIGFSFVPSSTFTSSSTYT 300
QY 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
DB 291 SCDSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTGPPASTHLCTGPPASTHLCT 350
QY 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATL-----ASDPIP 335
DB 301 PGDCPNF---AAPREVAAPYOGADPIL-----ATL-----ASDPIP 335
QY 351 TPVQKWEASAPAPQADADPATLYAVVDGVPSPRWKELVRRIGLSEHEIERLENGR 410
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Db 336 NPLQWESDA-HKQSLDTDDPATLYAVAVENVPPLRMKEFVRRLGSLSDHEIDRLQNGR 394  
Qy 411 HUREAQSMLAAMRRRTPRREATLELLGRVLRDMDLGLCLENIEBEALGAARLASBPRL 470  
Db 395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLGLCLENIEBEALGPALPAPBPRL 454

## RESULT 12

US-09-898-234-2  
Sequence 2, Application US/09898234  
Patent No. US2002015112A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stralow, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98,385-1  
CURRENT FILING DATE: 2001-07-03  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 09/525,998  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-898-234-2

Query Match 58.3%; Score 1517; DB 10; Length 455;  
Best Local Similarity 62.9%; Pred. No. 7.1e-101;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;  
Qy 1 MGLPTVPGLLLPLVLPALLADVPAGVGLVPHPGDEKESPPCKGKYNHPONSTICT 60  
Db 1 MGLSTVDLLPLVLLVLLVGLVPSGVGLVPHGLDEKSDVCPQKTIHPONNSICT 60  
Qy 61 KCHGTYLYNDPCPGQDTPDCRECGSGFTASENHLRHCLSCSKCKEMGVVEISSCTVD 120  
Db 61 KCHGTYLYNDPCPGQDTPDCRECGSGFTASENHLRHCLSCSKCKEMGVVEISSCTVD 120  
Qy 121 RDTVCGCKRQRYRYNMGEGTGRCLNCSLCPRNGTYNIPCOERODITCHGMGFPLKAKCI 180  
Db 121 RDTVCGCKRQRYRYNMGEGTGRCLNCSLCPRNGTYNIPCOERODITCHGMGFPLKAKCI 180  
Qy 121 RDTVCGCKRQRYRYNMGEGTGRCLNCSLCPRNGTYNIPCOERODITCHGMGFPLKAKCI 180  
Db 121 RDTVCGCKRQRYRYNMGEGTGRCLNCSLCPRNGTYNIPCOERODITCHGMGFPLKAKCI 180  
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Db 181 SCHDCKNK-ECEKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCASFASVYLACRYORWK 239  
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Db 181 SCNSCKSLBETKLCPLQIENVKGTEDSGTTVLLPLVIFGLCLSLFLIGLMTRYORWK 240  
Qy 240 PKLYSIICGOSTLVKSGEP-----LLVPAFGFNP-----TTTICFSSSTPSSSPVSIPIYI 290  
Db 240 PKLYSIICGOSTLVKSGEP-----LLVPAFGFNP-----TTTICFSSSTPSSSPVSIPIYI 290  
Qy 241 SKLYSIIVCGKSTPEKEGELBETTTKPLAPNPSFSPTPGFTPLGFSVPSSSTFTSSSTYT 300  
Db 241 SKLYSIIVCGKSTPEKEGELBETTTKPLAPNPSFSPTPGFTPLGFSVPSSSTFTSSSTYT 300  
Qy 291 SCDSNFGAIVASPSSETAPPLKAGPILPGRPASHTLCTGPPASHTLCTGPPASHTLC 350  
Db 291 SCDSNFGAIVASPSSETAPPLKAGPILPGRPASHTLCTGPPASHTLCTGPPASHTLC 350  
Qy 301 PGDCPNF---AAPREVAAPPQADPIL-----ATAL-----ASDPIP 335  
Db 301 PGDCPNF---AAPREVAAPPQADPIL-----ATAL-----ASDPIP 335  
Qy 351 TPVQKWEASAPASADQADADPATLYAVAVDGPSPRMKELVRLGLSEHIEIRLENGR 410  
Db 351 TPVQKWEASAPASADQADADPATLYAVAVDGPSPRMKELVRLGLSEHIEIRLENGR 410  
Qy 336 NPLQWESDA-HKQSLDTDDPATLYAVAVENVPPLRMKEFVRRLGSLSDHEIDRLQNGR 394  
Db 336 NPLQWESDA-HKQSLDTDDPATLYAVAVENVPPLRMKEFVRRLGSLSDHEIDRLQNGR 394  
Qy 411 HUREAQSMLAAMRRRTPRREATLELLGRVLRDMDLGLCLENIEBEALGAARLASBPRL 470  
Db 411 HUREAQSMLAAMRRRTPRREATLELLGRVLRDMDLGLCLENIEBEALGAARLASBPRL 470

Db 395 CLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLGLCLENIEBEALGPALPAPBPRL 454

## RESULT 13

US-09-898-234-17  
Sequence 17, Application US/09898234  
Patent No. US2002015112A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stralow, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98,385-1  
CURRENT FILING DATE: 2001-07-03  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 09/525,998  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Description of Artificial Sequence: human TNF-R in  
OTHER INFORMATION: ITNF-R2  
US-09-898-234-17

Query Match 58.3%; Score 1517; DB 10; Length 455;  
Best Local Similarity 62.9%; Pred. No. 7.1e-101;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;  
Qy 1 MGLPTVPGLLLPLVLPALLADVPAGVGLVPHPGDEKESPPCKGKYNHPONSTICT 60  
Db 1 MGLSTVDLLPLVLLVLLVGLVPSGVGLVPHGLDEKSDVCPQKTIHPONNSICT 60  
Qy 61 KCHGTYLYNDPCPGQDTPDCRECGSGFTASENHLRHCLSCSKCKEMGVVEISSCTVD 120  
Db 61 KCHGTYLYNDPCPGQDTPDCRECGSGFTASENHLRHCLSCSKCKEMGVVEISSCTVD 120  
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Db 121 RDTVCGCKRQRYRYNMGEGTGRCLNCSLCPRNGTYNIPCOERODITCHGMGFPLKAKCI 180  
Qy 121 RDTVCGCKRQRYRYNMGEGTGRCLNCSLCPRNGTYNIPCOERODITCHGMGFPLKAKCI 180  
Db 121 RDTVCGCKRQRYRYNMGEGTGRCLNCSLCPRNGTYNIPCOERODITCHGMGFPLKAKCI 180  
Qy 181 SCHDCKNK-ECEKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCASFASVYLACRYORWK 239  
Db 181 SCHDCKNK-ECEKLCPTRPSTGKDSODPGTTVLLPLVIVFGLCASFASVYLACRYORWK 239  
Qy 181 SCNSCKSLBETKLCPLQIENVKGTEDSGTTVLLPLVIFGLCLSLFLIGLMTRYORWK 240  
Db 181 SCNSCKSLBETKLCPLQIENVKGTEDSGTTVLLPLVIFGLCLSLFLIGLMTRYORWK 240  
Qy 240 PKLYSIICGOSTLVKSGEP-----LLVPAFGFNP-----TTTICFSSSTPSSSPVSIPIYI 290  
Db 240 PKLYSIICGOSTLVKSGEP-----LLVPAFGFNP-----TTTICFSSSTPSSSPVSIPIYI 290  
Qy 241 SKLYSIIVCGKSTPEKEGELBETTTKPLAPNPSFSPTPGFTPLGFSVPSSSTFTSSSTYT 300  
Db 241 SKLYSIIVCGKSTPEKEGELBETTTKPLAPNPSFSPTPGFTPLGFSVPSSSTFTSSSTYT 300  
Qy 291 SCDSNFGAIVASPSSETAPPLKAGPILPGRPASHTLCTGPPASHTLCTGPPASHTLC 350  
Db 291 SCDSNFGAIVASPSSETAPPLKAGPILPGRPASHTLCTGPPASHTLCTGPPASHTLC 350  
Qy 301 PGDCPNF---AAPREVAAPPQADPIL-----ATAL-----ASDPIP 335  
Db 301 PGDCPNF---AAPREVAAPPQADPIL-----ATAL-----ASDPIP 335  
Qy 351 TPVQKWEASAPASADQADADPATLYAVAVDGPSPRMKELVRLGLSEHIEIRLENGR 410  
Db 351 TPVQKWEASAPASADQADADPATLYAVAVDGPSPRMKELVRLGLSEHIEIRLENGR 410  
Qy 336 NPLQWESDA-HKQSLDTDDPATLYAVAVENVPPLRMKEFVRRLGSLSDHEIDRLQNGR 394  
Db 336 NPLQWESDA-HKQSLDTDDPATLYAVAVENVPPLRMKEFVRRLGSLSDHEIDRLQNGR 394  
Qy 411 HUREAQSMLAAMRRRTPRREATLELLGRVLRDMDLGLCLENIEBEALGAARLASBPRL 470  
Db 411 HUREAQSMLAAMRRRTPRREATLELLGRVLRDMDLGLCLENIEBEALGAARLASBPRL 470

Db 395 CLREAQVSMLATWRRRTPREATLELLGRVLRDMDLGLCLEDIEBALCGPALPPAPSL 454

RESULT 14  
US-09-756-854-5  
Sequence 5, Application US/09756854  
Patent No. US20020164684A1  
GENERAL INFORMATION:  
APPLICANT: NI, Jian  
Yu, Guo-Liang  
Fan, Ping  
Gentz, Reiner  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/756,854  
FILING DATE: 10-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/095,094  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoover, Kenley K.  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PF375  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-756-854-5

Query Match 58.3%; Score 1517; DB 10; Length 455;  
Best Local Similarity 62.9%; Pred. No. 7,1e-101;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPGLLPLVLPALADVPAGVGLVPHPDLEKRESPPCGKYNHPNSTICT 60  
Db 1 MGLSTVPLDLLPLVLELVGIVPSGVGLVPHLDREKRSVCGKYNHPNSTICT 60  
Qy 61 KCHKGTLYNDCPGRGRTDRCVCAPTVTALNHLRRLCSRCRDEMFOVEISPCVVD 120  
Db 61 KCHKGTLYNDCPGRGRTDRCVCAPTVTALNHLRRLCSRCRDEMFOVEISPCVVD 120  
Qy 121 RDTVCGCKNOYREWGETGFRCLNCSLCPNGTNIIPCOERODTICHGMGFFLGAKCI 180  
Db 121 RDTVCGCKNOYREWGETGFRCLNCSLCPNGTNIIPCOERODTICHGMGFFLGAKCI 180  
Qy 181 SCHDCKN-EECKLCPTRPSTGKSDQDPGTTVLLPLVIVFGCLASFPASVVLACRYQRMK 239  
Db 181 SCHDCKN-EECKLCPTRPSTGKSDQDPGTTVLLPLVIVFGCLASFPASVVLACRYQRMK 239  
Qy 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSTPSSSPVSIPIYI 290  
Db 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSTPSSSPVSIPIYI 290  
Qy 241 SKLYSIVCGKSTPEKEGLEGTTRTKPLAPNPSFPTPGFTPLGFSVPVSSSTFTSSSTYT 300  
Db 241 SKLYSIVCGKSTPEKEGLEGTTRTKPLAPNPSFPTPGFTPLGFSVPVSSSTFTSSSTYT 300

Qy 291 SCDNSNFGAVASPSSETAPPHLKAGPILGPPASTHLCCTGPPASTHLCCTGPPASTHLC 350  
Db 301 PGDCPNF---AAPREVAPPYQADPIL-----ATAL-----ASDPIP 335  
Qy 351 TPVQKWEASAPSDQDLADADPATLYAVVDVPSRWKELVRLGLSEHIEIRLENGR 410  
Db 336 NPLQKWEASA-HKQSLDTDDPATLYAVVENVPPLRWKEFVRRIGLSDEHIDRLQLQGR 394  
Qy 411 HLEEAQVSMLATWRRRTPREATLELLGRVLRDMDLGLCLEDIEBALCGPALPPAPSL 470  
Db 395 CLREAQVSMLATWRRRTPREATLELLGRVLRDMDLGLCLEDIEBALCGPALPPAPSL 454

RESULT 15  
US-09-899-429A-2  
Sequence 2, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Himmeler, Rudolph  
Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-899-429A-2

Query Match 58.3%; Score 1517; DB 10; Length 455;  
Best Local Similarity 62.9%; Pred. No. 7,1e-101;  
Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

Qy 1 MGLPTVPGLLPLVLPALADVPAGVGLVPHPDLEKRESPPCGKYNHPNSTICT 60  
Db 1 MGLSTVPLDLLPLVLELVGIVPSGVGLVPHLDREKRSVCGKYNHPNSTICT 60  
Qy 61 KCHKGTLYNDCPGRGRTDRCVCAPTVTALNHLRRLCSRCRDEMFOVEISPCVVD 120  
Db 61 KCHKGTLYNDCPGRGRTDRCVCAPTVTALNHLRRLCSRCRDEMFOVEISPCVVD 120  
Qy 121 RDTVCGCKNOYREWGETGFRCLNCSLCPNGTNIIPCOERODTICHGMGFFLGAKCI 180  
Db 121 RDTVCGCKNOYREWGETGFRCLNCSLCPNGTNIIPCOERODTICHGMGFFLGAKCI 180  
Qy 181 SCHDCKN-EECKLCPTRPSTGKSDQDPGTTVLLPLVIVFGCLASFPASVVLACRYQRMK 239  
Db 181 SCHDCKN-EECKLCPTRPSTGKSDQDPGTTVLLPLVIVFGCLASFPASVVLACRYQRMK 239  
Qy 240 PKLYSIICGOSTLVKEGPE-----LVVAPGFNP-----TTTICSSTPSSSPVSIPIYI 290  
Db 241 SKLYSIVCGKSTPEKEGLEGTTRTKPLAPNPSFPTPGFTPLGFSVPVSSSTFTSSSTYT 300  
Qy 241 SCDNSNFGAVASPSSETAPPHLKAGPILGPPASTHLCCTGPPASTHLCCTGPPASTHLC 350

Db	301	PGDCPNF--AAPRREVA	PPYOGADPIL	-----	ATAL	-----	ASDP	PIP	335
Qy	351	TPVQKWEASAP	SAPDQADPATLYAV	VDGVP	PPSRWKELV	RRI	GLSEHEIER	LENGR	410
Db	336	NPLQKWE	SDA-HKQSLD	TDDPATLYAV	VENVPL	RWKEF	VRRIGLSD	HEIDRELE	ONGR 394
Qy	411	HLREAOYS	MLAAMRRRT	PPREATT	ELIGRV	LRDMDL	GCLENIE	BALGAAR	LASEPRL 470
Db	395	CLREAOYS	MLATWRRT	TPREATT	ELIGRV	LRDMDL	GCLEDB	IBALCG	PAALPPAPSL 454

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 Job time : 28 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2003, 07:02:24 ; Search time 20 Seconds

(without alignments)  
2264.772 Million cell updates/sec

Title: US-09-970-532-2

Perfect score: 2603  
Sequence: 1 MGLPTVPGLLPLVLPALLA.....NIEBALGCAARLASPPRLW 471

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1750	67.2	461	2	JC4302 tumor necrosis fac
2	1517	58.3	455	1	GQHUT1 tumor necrosis fac
3	1338.5	51.4	461	1	GQRTH1 tumor necrosis fac
4	1319	50.7	454	1	GQNST1 tumor necrosis fac
5	257	9.9	435	2	IS4182 tumor necrosis fac
6	236	9.1	427	1	GQHUN tumor necrosis fac
7	227.5	8.7	425	1	A26431 nerve growth facto
8	220	8.5	416	1	UN0006 nerve growth facto
9	199.5	7.7	451	2	JC7705 death receptor-6
10	199	7.6	461	1	A35356 tumor necrosis fac
11	193	7.4	595	2	A42086 CD30 antigen precu
12	181.5	7.0	324	2	JC2395 Fas antigen precu
13	181.5	7.0	325	2	B43692 T2 protein - rabbi
14	180	6.9	326	1	GOVZML T2 protein - myxom
15	178.5	6.9	474	2	B38634 tumor necrosis fac
16	173	6.6	459	2	I48854 gene murine tumour
17	169	6.5	3635	2	T10053 laminin alpha 5 ch
18	168.5	6.5	305	2	A46476 B cell-associated
19	163.5	6.3	348	2	J28623 hypothetical prote
20	163.5	6.3	349	2	D72175 G2R protein - vari
21	163.5	6.3	349	2	D36858 gene GAR protein
22	161	6.2	327	2	A46484 apoptosis-mediatin
23	155	6.0	1548	2	S34583 serine proteinase
24	150	5.8	1613	2	J50272 low density lipopr
25	149	5.7	1613	2	J50273 laminin beta-2 cha
26	147.5	5.7	1801	1	NRRTS apoptosis-mediatin
27	147	5.6	335	2	A40036 notch3 protein - h
28	147	5.6	2321	2	S78549 furin (EC 3.4.21.7
29	145.5	5.6	1299	2	T43251

30	145	5.6	260	1	A46517 CD27 antigen precu
31	142.5	5.5	1639	1	NMFR2 laminin gamma-1 ch
32	141.5	5.4	915	2	B48225 probable proteol
33	140.5	5.4	1111	2	T26972 hypothetical prote
34	140.5	5.4	1513	2	A54895 mucin 2, intestina
35	140.5	5.4	3020	2	A43932 mucin 2 precursor,
36	140	5.4	277	2	I37552 OX40 homolog - hum
37	140	5.4	1797	2	A55677 laminin beta-2 cha
38	139.5	5.4	3672	2	T23433 hypothetical prote
39	139.5	5.4	3704	2	T73316 probable laminin a
40	138.5	5.3	915	1	A48225 subtilisin-like pr
41	138	5.3	5262	2	T03454 AAR protein - huma
42	137.5	5.3	1574	2	T13954 MGCF6 protein - ra
43	137.5	5.3	5376	2	T42215 zonadhesin - mouse
44	136	5.2	826	2	A60385 monocyste surface a
45	135.5	5.2	937	2	I53282 gene PAC4 protein

## ALIGNMENTS

## RESULT 1

JC4302 tumor necrosis factor receptor p55 precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999

C:Accession: JC4302; PC4093

R:Stuer, B.; Pauli, U.

Gene 163, 263-266, 1995

A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

A:Reference number: JC4302; MUID:96011645; PMID:7590278

A:Accession: JC4302

A:Molecule type: mRNA

A:Residues: 1-461 <SU2>

A:Cross-references: GB:U19994; NID:g1141752; PIDN:AN048499.1; PID:g1141753

A:Accession: PC4093

A:Molecule type: protein

A:Residues: 1-7 <SU2>

A:Experimental source: kidney cell line 15

C:Genetics:

A:Gene: tnfr

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor

F:1-29/Domin: signal sequence #status predicted <SIG>

F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>

F:44-194/Domin: extracellular cysteine rich #status predicted <EXT>

F:84-126/Domin: NGF receptor repeat homology <NGF>

F:211-231/Domin: transmembrane #status predicted <TM>

F:361-447/Domin: signal transduction #status predicted <ST>

F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.2% Score 1750; DB 2; Length 461;

Best Local Similarity 70.2% Pred. No. 6.5e-100;

Matches 339; Conservative 24; Mismatches 84; Indels 36; Gaps 5;

QY	1	MGLPTVPGLLPLVLPALLADVPAVGVLVPHGDLKRRSPPOGKVNPNSTICT	60
DB	1	MGLSTVPGLLPLVLPALLADVPAVGVLVPHGDLKRRSLCPQGKSHPNRSICT	60
QY	61	KCHGTYLVNDPCPGRDTCGVCAPGTATLENHLRRCSCSRDEMPVEVSPCVVD	120
DB	61	KCHGTYLVNDPCPGDTCGVCAPGTATLENHLRRCSCSRDEMPVEVSPCVVD	120
QY	121	RDYTCGCRKQYRYWGTGRCNLGCLCPNGTINIPCOERODITICCHMGFLKAKCI	180
DB	121	RDYTCGCRKQYRYWGTGRCNLGCLCPNGTINIPCOERODITICCHMGFLKAKCI	180
QY	181	SCHDCKKECEKLCPTPSTGKSDQPGTTLPLVIVFGCLASFASVVLACGYORKKP	240
DB	181	SCVCKKADCKNLCPATSETRNDPQDTGTYLPLVIVFGCLASFPLVGLACGYORKKP	240
QY	241	KLVSIIIGOSTLVKGEPELLVPAFGNPPTTI-----CFSSTPSSSPVSIPIPI	290

Db 241 KLVSTICGKSTVXKGEPEPLATAPSPGPITTFSPSPPTTSSPVSPSPISPFPT 300  
 Qy 231 SCDRNFCAVAPSPSETAPPHKAGPILFGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350  
 Db 301 PCDMGNI-KVSPSPKEIAPPPGAGPILPMPAS-----TPVP----- 337  
 Qy 351 TPVQKMEA---SAPAPDQADADPATLYAVVDGVPSPKWEKLVRLGSEHEIRLELE 407  
 Db 338 TPLPMGSAHSAHAPQADADPATLYAVVDGVPSPKWEKLVRLGSEHEIRLELE 397  
 Qy 408 NGRHLREAOYSLAAMRRRTPRREATLELGLVRLDMDLGLCLENIEEALGGAARLASEP 467  
 Db 398 NGRCLREAOYSLAAMRRRTSRREATLELGLVRLDMDLGLCLENIEEALGGAARLASEP 457  
 Qy 468 RLL 470  
 Db 458 HLL 460

RESULT 2  
 tumor necrosis factor receptor 1 precursor [validated] - human  
 N/Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1  
 N/Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Jun-1997 #sequence revision 30-Jun-1992 #text change 08-Dec-2000  
 C/Accession: A38208; A34899; A39900; A36555; A38281; S12057; J07058; A60231; A38  
 R/Gene: P. Strehl, S.; Dwozrak, M.; Himmler, A.; Ambrose, P.F.  
 A/Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to ch  
 A/Reference number: A38208; MUID:92250049; PMID:1315717  
 A/Accession: A38208

A/Molecule type: DNA  
 A/Residues: 1-455 <FUC>  
 A/Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:G339748; PIDN:AAA61201.1; PID:G  
 R/Schall, T.J.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau  
 Cell 61, 351-359, 1990  
 A/Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep  
 A/Reference number: A34899; MUID:90235284; PMID:2158862  
 A/Accession: A34899

A/Molecule type: mRNA  
 A/Residues: 1-455 <LOB>  
 A/Cross-references: GB:M58286; GB:M3480; NID:G339753; PIDN:AAA36753.1; PID:G339754  
 A/Note: part of this sequence, including the amino end of the mature protein, confirmed  
 R/Schall, T.J.; Lewis, M.; Koller, K.D.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.  
 Cell 61, 361-370, 1990  
 A/Title: Molecular cloning and expression of a receptor for human tumor necrosis factor  
 A/Reference number: A34900; MUID:90235285; PMID:2158863  
 A/Accession: A34900

A/Molecule type: mRNA  
 A/Residues: 1-455 <SCH>  
 A/Cross-references: GB:M3294; NID:G339744; PIDN:AAA03210.1; PID:G339745  
 R/Himmler, A.; Mauey-Fogay, I.; Kroenke, M.; Scheutrich, P.; Pfizenmaier, K.; Lantz, M.;  
 DNA Cell Biol. 9, 705-715, 1990  
 A/Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto  
 A/Reference number: A36555; MUID:91090841; PMID:1702293  
 A/Accession: A36555

A/Molecule type: mRNA  
 A/Residues: 1-455 <HIM>  
 A/Cross-references: GB:M63121; NID:G339755; PIDN:AAA36754.1; PID:G339756  
 A/Accession: C36555

A/Molecule type: protein  
 A/Residues: 30-38/41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104/107-128/162-167, 'X', 169-2  
 A/Note: the purified protein, called tumor necrosis factor binding protein, is a soluble  
 R/Grey, P.W.; Barrett, K.; Chaney, D.; Turner, M.; Feldmann, M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990  
 A/Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re  
 A/Reference number: A38281; MUID:91017509; PMID:2170974  
 A/Accession: A38281

A/Molecule type: mRNA  
 A/Residues: 1-455 <GRA>

A/Cross-references: GB:M37764  
 A/Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
 R/Nopar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zhang, R.; Aderka, D.; Holtmann,  
 EMBO J. 9, 3269-3278, 1990  
 A/Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type  
 I form of the receptor.  
 A/Reference number: S12057; MUID:91060021; PMID:1698610  
 A/Accession: S12057

A/Molecule type: mRNA  
 A/Residues: 1-455 <NOP>  
 A/Cross-references: EMBL:X55313; NID:G37223; PIDN:CAA39021.1; PID:G37224  
 A/Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, we  
 R/Kemper, O.; Wallach, D.  
 Gene 134, 209-216, 1993  
 A/Title: Cloning and partial characterization of the promoter for the human p55 tumor nec  
 A/Reference number: J07058; MUID:94085779; PMID:8262379  
 A/Accession: J07058

A/Molecule type: DNA  
 A/Residues: 1-13 <KEM>  
 R/Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
 Eur. J. Immunol. 20, 1167-1174, 1990  
 A/Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence  
 A/Reference number: A60231; MUID:90292116; PMID:2113477  
 A/Accession: A60231

A/Molecule type: protein  
 A/Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>  
 R/Gatanaga, T.; Huang, C.; Kohr, W.; Capuccini, F.; Lucif III, J.A.; Jeffrey, E.W.B.; Let  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
 A/Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto  
 A/Reference number: A38258; MUID:91062364; PMID:2174164  
 A/Accession: A38258

A/Molecule type: protein  
 A/Residues: 41-60 <GAT>  
 A/Experimental source: cancer patient serum  
 R/Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyrell, H.; Grubb, A.; Adolf, G.  
 Eur. J. Haematol. 42, 270-275, 1989  
 A/Title: Isolation and characterization of a tumor necrosis factor binding protein from  
 A/Reference number: A60594; MUID:89171156; PMID:2924890  
 A/Accession: A60594

A/Molecule type: protein  
 A/Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XX', 60 <OLS>  
 A/Experimental source: renal failure patient urine  
 R/Engelmann, H.; Novick, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A/Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence f  
 A/Reference number: A35010; MUID:90110215; PMID:2153136  
 A/Accession: A35010

A/Molecule type: protein  
 A/Residues: 41-45 <ENG>  
 A/Experimental source: normal urine  
 R/Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
 Bioessl. Biotechnol. Biochem. 58, 2266-2268, 1994  
 A/Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified fr  
 A/Reference number: J02404; MUID:95128033; PMID:7765720  
 A/Accession: J02404

A/Molecule type: protein  
 A/Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAL>  
 A/Experimental source: urine  
 C/Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
 C/Genetics:  
 A/Gene: GDB:TNFR1  
 A/Cross-references: GDB:125913; OMIM:191190  
 A/Map position: 12p13.2-12p13.2  
 A/Intons: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
 C/Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C/Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
 F:30-211/Domain: extracellular #status predicted <EXT>  
 F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
 F:44-82/Domain: NGF receptor repeat homology <NG1>  
 F:84-126/Domain: NGF receptor repeat homology <NG2>

F:127-167/Domain: NGF receptor repeat homology <NG3>  
 F:168-196/Domain: NGF receptor repeat homology <NG4>  
 F:212-234/Domain: transmembrane #status predicted <MEM>  
 F:234-455/Domain: intracellular #status predicted <INT>  
 F:254-145/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.3%; Score 1517; DB 1; Length 455;  
 Best Local Similarity 62.9%; Pred. No. 1,1e-85;  
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;

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QY 1 MGSLPTVGLLPLVLPALLADVPAGVQGLVPHRGDLKRESPCPQKXNHPQNSTICT 60
DB 1 MGSLPTVGLLPLVLPALLADVPAGVQGLVPHRGDLKRESPCPQKXNHPQNSTICT 60
QY 61 KCHKGTVLYNDPCPGRDTCRCVCAPTVTALBNHLRCLSCSRCDPDMFOVEISPCVD 120
DB 61 KCHKGTVLYNDPCPGRDTCRCVCAPTVTALBNHLRCLSCSRCDPDMFOVEISPCVD 120
QY 121 RDTVCGCRKNQYREYWGTEGFRCLNSLCPNGVTNIPQERODITICHGMGFLKAKCI 180
DB 121 RDTVCGCRKNQYREYWGTEGFRCLNSLCPNGVTNIPQERODITICHGMGFLKAKCI 180
QY 181 SCHDCKRK-ECEKLCPTRPSTGKDSODPGTTLPLVTVGGLCLASPAVVLACRYORWK 239
DB 181 SCHDCKRK-ECEKLCPTRPSTGKDSODPGTTLPLVTVGGLCLASPAVVLACRYORWK 239
QY 240 PKLYSIICGOSTLVKEGEP-----LVPAPGPNP-----TTTICFSSSTPSSPVSIPIYI 290
DB 240 PKLYSIICGOSTLVKEGEP-----LVPAPGPNP-----TTTICFSSSTPSSPVSIPIYI 290
QY 291 SCDSNFGAVASPSSETAPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
DB 291 SCDSNFGAVASPSSETAPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
QY 301 PGDCPNP-----AAPREVAPPYGADPIL-----ATML-----ASPPIF 335
DB 301 PGDCPNP-----AAPREVAPPYGADPIL-----ATML-----ASPPIF 335
QY 351 TPVQKWEASASAPDQADADPATLYAVNDGVPSPRKEVLVRGLSGHEIERLENGR 410
DB 351 TPVQKWEASASAPDQADADPATLYAVNDGVPSPRKEVLVRGLSGHEIERLENGR 410
QY 336 NPLQKWEKDSA-HKQOSLDTDDPATLYAVENVPLRKEVPRRLGSLDHEIDRELONGR 394
DB 336 NPLQKWEKDSA-HKQOSLDTDDPATLYAVENVPLRKEVPRRLGSLDHEIDRELONGR 394
QY 411 HLREAOYSMLAMPRRTPREATTLELGRVLRDMDLGLCLNIEBALGGAARLASEPRL 470
DB 411 HLREAOYSMLAMPRRTPREATTLELGRVLRDMDLGLCLNIEBALGGAARLASEPRL 470
QY 395 CLRBAQYSMLATWRRTRRRTREATTLELGRVLRDMDLGLCLNIEBALGGAARLASEPRL 454
DB 395 CLRBAQYSMLATWRRTRRRTREATTLELGRVLRDMDLGLCLNIEBALGGAARLASEPRL 454

```

## RESULT 3

GOMST1  
 tumor necrosis factor receptor 1 precursor - rat

C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 22-Jun-1999

R:Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pitzemaier, K.; Lantz, M.;  
 DNA Cell Biol. 9, 705-715, 1990

A/Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor  
 A/Reference number: A36555; MUID:91090841; PMID:1702293

A/Accession: B36555  
 A/Molecule type: mRNA

A/Residues: 1-461 <HM>  
 A/Cross-references: GB:M63122; NID:9207361; PIDN:AAA42256.1; PID:9207362

C/Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
 C/Supersfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C/Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
 F:30-211/Domain: extracellular #status predicted <EXT>

F:30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>  
 F:44-82/Domain: NGF receptor repeat homology <NG3>

F:84-126/Domain: NGF receptor repeat homology <NG2>  
 F:127-167/Domain: NGF receptor repeat homology <NG4>

F:168-204/Domain: NGF receptor repeat homology <NG4>  
 F:212-234/Domain: transmembrane #status predicted <MEM>

F:234-461/Domain: intracellular #status predicted <INT>  
 F:54-151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.4%; Score 1338.5; DB 1; Length 461;  
 Best Local Similarity 55.8%; Pred. No. 9.2e-75;  
 Matches 268; Conservative 51; Mismatches 114; Indels 47; Gaps 9;

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QY 1 MGSLPTVGLLPLVLPALLADVPAGVQGLVPHRGDLKRESPCPQKXNHPQNSTICT 60
DB 1 MGSLPTVGLLPLVLPALLADVPAGVQGLVPHRGDLKRESPCPQKXNHPQNSTICT 60
QY 61 KCHKGTVLYNDPCPGRDTCRCVCAPTVTALBNHLRCLSCSRCDPDMFOVEISPCVD 120
DB 61 KCHKGTVLYNDPCPGRDTCRCVCAPTVTALBNHLRCLSCSRCDPDMFOVEISPCVD 120
QY 121 RDTVCGCRKNQYREYWGTEGFRCLNSLCPNGVTNIPQERODITICHGMGFLKAKCI 180
DB 121 RDTVCGCRKNQYREYWGTEGFRCLNSLCPNGVTNIPQERODITICHGMGFLKAKCI 180
QY 181 SCHDCKRK-ECEKLCPTRPSTGKDSODPGTTLPLVTVGGLCLASPAVVLACRYORWK 239
DB 181 SCHDCKRK-ECEKLCPTRPSTGKDSODPGTTLPLVTVGGLCLASPAVVLACRYORWK 239
QY 240 PKLYSIICGOSTLVKEGEP-----LVPAPGPNP-----TTTICFSSSTPSSPVSIPIYI 290
DB 240 PKLYSIICGOSTLVKEGEP-----LVPAPGPNP-----TTTICFSSSTPSSPVSIPIYI 290
QY 291 SCDSNFGAVASPSSETAPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
DB 291 SCDSNFGAVASPSSETAPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
QY 301 PGDCPNP-----AAPREVAPPYGADPIL-----ATML-----ASPPIF 335
DB 301 PGDCPNP-----AAPREVAPPYGADPIL-----ATML-----ASPPIF 335
QY 343 P-PASTHLCTPVQKWEASASAPDQADADPATLYAVNDGVPSPRKEVLVRGLSGHEIERLENGR 401
DB 343 P-PASTHLCTPVQKWEASASAPDQADADPATLYAVNDGVPSPRKEVLVRGLSGHEIERLENGR 401
QY 339 PIPA-----PVRKEVAVAAQFORLDTADPAKLYAVNDGVPSPRKEVLVRGLSGHEIERLENGR 392
DB 339 PIPA-----PVRKEVAVAAQFORLDTADPAKLYAVNDGVPSPRKEVLVRGLSGHEIERLENGR 392
QY 402 ERLELENGRHLREAOYSMLAMPRRTPREATTLELGRVLRDMDLGLCLNIEBALGGAARLASEPRL 461
DB 402 ERLELENGRHLREAOYSMLAMPRRTPREATTLELGRVLRDMDLGLCLNIEBALGGAARLASEPRL 461
QY 393 ERLELENGRHLREAOYSMLAMPRRTPREATTLELGRVLRDMDLGLCLNIEBALGGAARLASEPRL 452
DB 393 ERLELENGRHLREAOYSMLAMPRRTPREATTLELGRVLRDMDLGLCLNIEBALGGAARLASEPRL 452

```

## RESULT 4

GOMST1  
 tumor necrosis factor receptor 1 precursor - mouse

N/Alternate names: tumor necrosis factor receptor, 55K  
 C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 01-Dec-2000  
 C/Accession: A38634; B40254; S16677; S19021; S4543; S57826

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A/Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r  
 A/Reference number: A38634; MUID:91187885; PMID:1849278

A/Accession: A38634  
 A/Molecule type: mRNA

A/Residues: 1-454 <LEW>  
 A/Cross-references: GB:M60468; NID:919825; PIDN:AAA39751.1; PID:919826

R:Goodwin, R.G.; Anderson, D.; Jexy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk  
 Mol. Cell. Biol. 11, 3020-3026, 1991

A/Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for t  
 A/Reference number: A40254; MUID:91246168; PMID:1645445

A/Accession: B40254  
 A/Molecule type: mRNA

A/Residues: 1-454 <GG2>  
 A/Cross-references: GB:M60468; NID:919825; PIDN:AAA39751.1; PID:919826

R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissebergh, A.M.; Gray, P.W.; Feldmar  
 Eur. J. Immunol. 21, 1649-1656, 1991

A/Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis  
 A/Reference number: S16677; MUID:91285014; PMID:1647956

A/Accession: S16677  
 A/Molecule type: mRNA

A/Residues: 1-454 <BAR>  
 A/Cross-references: EMBL:X59238; NID:953578; PIDN:CAA41922.1; PID:953579

R:Roche, J.G.; Brockhaus, M.; Gentz, R.; Lieselauer, W.  
 Immunogenetics 34, 338-340, 1991

A/Title: Molecular cloning and expression of the mouse Tnf receptor type b.  
 A/Reference number: S19021; MUID:92039815; PMID:1657766  
 A/Accession: S19021

A:Molecule type: mRNA  
 A:Residues: 1-454 <ROT>  
 A:Cross-references: EMBL:X57796; NID:G54848; PIDN:CAA40936.1; PID:G54849  
 R:Bebo, B.P.  
 Immunogenetics 39, 450-451, 1994  
 A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1  
 A:Reference number: 154532; MUID:94245292; PMID:8188324  
 A:Accession: 154532  
 A:Molecule type: mRNA  
 A:Status: translated from GB/EMBL/DBJ  
 A:Residues: 1-454 <RES>  
 A:Cross-references: GB:I26349; NID:G430732; PIDN:AAA59361.1; PID:G430733  
 R:Rothe, J.G.; Bluetmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.  
 Mol. Immunol. 30, 165-176, 1993  
 A:Title: Genome organization and promoter function of the murine tumor necrosis factor  
 A:Reference number: 157826; MUID:93156721; PMID:8381516  
 A:Accession: 157826  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-393; G', 395-454 <RES>  
 A:Cross-references: GB:M76566; NID:G202100; PIDN:AAA40465.1; PID:G202102  
 C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca  
 A:Gene: TNFR-2  
 A:Intron: 13/3, 65/1, 108/1, 158/1, 184/2, 210/1, 248/1, 257/3, 353/1  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei  
 F.1-29/Domain: signal sequence Helatius predicted <SIG>  
 F.30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
 F.30-212/Domain: extracellular Helatius predicted <EXT>  
 F.44-82/Domain: NGF receptor repeat homology <NG1>  
 F.84-126/Domain: NGF receptor repeat homology <NG2>  
 F.127-167/Domain: NGF receptor repeat homology <NG3>  
 F.168-204/Domain: NGF receptor repeat homology <NG4>  
 F.213-235/Domain: transmembrane #status predicted <MEM>  
 F.236-454/Domain: intracellular #status predicted <INT>  
 F.54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.7%; Score 1319; DB 1; Length 454;  
 Best Local Similarity 56.5%; Pred. No. 1,4e-73;  
 Matches 268; Conservative 55; Mismatches 109; Indels 42; Gaps 12;

```

OY 1 MGLPVPGLLLPLVLPALLADYVPAVOGLVPHPDLEKRESPPQGYKNHPONITICT 60
DB 1 MGLPVPGLLLPLVLPALLADYVPAVOGLVPHPDLEKRESPPQGYKNHPONITICT 60
OY 61 KCHKGTLYVNDGPGGRDTCRVCAPGYTALLENLRCLSGSRDDEMFOYEISPCYVD 120
DB 61 KCHKGTLYVNDGPGGRDTCRVCAPGYTALLENLRCLSGSRDDEMFOYEISPCYVD 120
OY 121 RDTVGGCRKNQYREYWGEGFRCLNCSLCPNGTVNI PCQERODTICHGMEFLGAKCI 180
DB 121 RDTVGGCRKNQYREYWGEGFRCLNCSLCPNGTVNI PCQERODTICHGMEFLGAKCI 180
OY 121 KDTVGGCKENQFORVLTSETHFCVDCSPFNGTVITPKETQNTVNCNCHAGFLRESQV 180
DB 121 KDTVGGCKENQFORVLTSETHFCVDCSPFNGTVITPKETQNTVNCNCHAGFLRESQV 180
OY 181 SCHDC-KKKECEKLC-PTRPSTGKDSORPGTIVLLPLVIVFGLCLASPAVVLACRYQRM 238
DB 181 SCHDC-KKKECEKLC-PTRPSTGKDSORPGTIVLLPLVIVFGLCLASPAVVLACRYQRM 238
OY 181 PCSHCKKNEECMKCLPPLPLAVNTNPOSGTAIVLLPLVILGLCLISLFIPLSLMKRYRWM 240
DB 181 PCSHCKKNEECMKCLPPLPLAVNTNPOSGTAIVLLPLVILGLCLISLFIPLSLMKRYRWM 240
OY 239 KPLYSIICGOSTLYKE---GEPELLVPAPGFNPT-----TICGSSSTSSSPVSIPIYIS 291
DB 239 KPLYSIICGOSTLYKE---GEPELLVPAPGFNPT-----TICGSSSTSSSPVSIPIYIS 291
OY 241 RPEVYSIICRDPVPVKEKAKGKPLTPASPAFSPISGNPFLGRTSTPGSSPVSSTP--- 297
DB 241 RPEVYSIICRDPVPVKEKAKGKPLTPASPAFSPISGNPFLGRTSTPGSSPVSSTP--- 297
OY 292 CDRSNGFVAVPSSETAPPLKAGPILPGPASTHLCTPG--PPASTHLCT-PPGPASTH 348
DB 292 CDRSNGFVAVPSSETAPPLKAGPILPGPASTHLCTPG--PPASTHLCT-PPGPASTH 348
OY 298 -----ISPIFGPSNW-----HFV-----PVSSEVVPVPGADPLLYESLCVPAV----- 336
DB 298 -----ISPIFGPSNW-----HFV-----PVSSEVVPVPGADPLLYESLCVPAV----- 336
OY 349 LCTPVQKKEASA-PPARPQLADADPATIYAVVDGVPBPKMKELVARLCLSEHEIFRLE 407
DB 349 LCTPVQKKEASA-PPARPQLADADPATIYAVVDGVPBPKMKELVARLCLSEHEIFRLE 407
OY 337 --TSVQKKEASAHPRPD--NADAILYAAVDGVPAPKMEFPMKFMELSHIEIRLEMQ 391
DB 337 --TSVQKKEASAHPRPD--NADAILYAAVDGVPAPKMEFPMKFMELSHIEIRLEMQ 391
OY 408 NGRHLREAYQSMILAMRRRTPREATYLELGRVLEDMMLCLCLEIIEALGAA 461
DB 408 NGRHLREAYQSMILAMRRRTPREATYLELGRVLEDMMLCLCLEIIEALGAA 461
OY 392 NGRCLREAYQSMILAMRRRTPREATYLELGRVLEDMMLCLCLEIIEALGAA 445
DB 392 NGRCLREAYQSMILAMRRRTPREATYLELGRVLEDMMLCLCLEIIEALGAA 445

```

RESULT 5  
 154182  
 tumor necrosis factor receptor 2-related protein - human  
 C:Species: Homo sapiens (man)  
 C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
 C:Accession: 154182  
 R:Baens, M.; Chalfant, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.  
 Genomics 16, 214-218, 1993  
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen  
 A:Reference number: 154182; MUID:99252381; PMID:8466360  
 A:Accession: 154182  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-435 <RES>  
 A:Cross-references: GB:L04270; NID:G339761; PIDN:AAA36757.1; PID:G339762  
 C:Gene: GDB:UTR  
 A:Cross-references: GDB:1230195; OMIM:600979  
 A:Map position: 12p13.3-12p13.1  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 9.9%; Score 257; DB 2; Length 435;  
 Best Local Similarity 27.3%; Pred. No. 1,1e-08;  
 Matches 121; Conservative 37; Mismatches 158; Indels 128; Gaps 25;

```

OY 1 MGLP---TVPGLLI-PLVLP--ALLADYVPAVOGLVPHPDLEKRESPPQGYKNHPON 54
DB 1 MGLP---TVPGLLI-PLVLP--ALLADYVPAVOGLVPHPDLEKRESPPQGYKNHPON 54
OY 55 STICCKHKTLYVNDGPGGRDTCRVCAPGYTALLENLRCLSGSRDDEMFOYEI 114
DB 55 STICCKHKTLYVNDGPGGRDTCRVCAPGYTALLENLRCLSGSRDDEMFOYEI 114
OY 56 -RCCSRCPPTVYSKAC-SRIKDTVCATCENSYNBNHNVLTTCQCRPCDPVWGLEEI 113
DB 56 -RCCSRCPPTVYSKAC-SRIKDTVCATCENSYNBNHNVLTTCQCRPCDPVWGLEEI 113
OY 115 SPQVVDRTVGGCRKNQYREYWGEGFRCLNCSL--CPNGTVNI PCQERODT----- 165
DB 115 SPQVVDRTVGGCRKNQYREYWGEGFRCLNCSL--CPNGTVNI PCQERODT----- 165
OY 114 APCTSKRTQCRCPGMFCAM---ALECTHCLSLSCPETE---ALEKDEYKGNH 166
DB 114 APCTSKRTQCRCPGMFCAM---ALECTHCLSLSCPETE---ALEKDEYKGNH 166
OY 166 -CHGMEFLK---GAKCISCHCKKKECKLCP---TRPSTGKSDP-----GT-- 209
DB 166 -CHGMEFLK---GAKCISCHCKKKECKLCP---TRPSTGKSDP-----GT-- 209
OY 167 CVPKAGHFONTSSPSARQDPHTRCENQGLVEAPGTAQSDPTTKNPLPRLPMSGTML 226
DB 167 CVPKAGHFONTSSPSARQDPHTRCENQGLVEAPGTAQSDPTTKNPLPRLPMSGTML 226
OY 210 --TVLPPLVIVFGCLASPAVVLACRYQRMKPLYSIICGOSTLYKEGPELLVPAPGF 267
DB 210 --TVLPPLVIVFGCLASPAVVLACRYQRMKPLYSIICGOSTLYKEGPELLVPAPGF 267
OY 227 MLAVLPLP--AFLLIATVFSI-----WKS--HSLCKLGLSKRPFQ-----GEGP 271
DB 227 MLAVLPLP--AFLLIATVFSI-----WKS--HSLCKLGLSKRPFQ-----GEGP 271
OY 268 NPTTTCFSSSTPSSSPVSIPIY-----ISCDRS--NFGAVASPSSETAPP----- 310
DB 268 NPTTTCFSSSTPSSSPVSIPIY-----ISCDRS--NFGAVASPSSETAPP----- 310
OY 272 NPV-----AGSWEPKAPHPDPLVQPLPIGSDVSPVSTGLPAPVLEAGVPOQOSP 324
DB 272 NPV-----AGSWEPKAPHPDPLVQPLPIGSDVSPVSTGLPAPVLEAGVPOQOSP 324
OY 311 -----HLKAGPLPVPASTHLCTPGP 332
DB 311 -----HLKAGPLPVPASTHLCTPGP 332
OY 325 LDLTREPOLBEREOSQVAHGTNGIHVTGSMITGNITLYNGPVLGGPBGDLPATPBP 384
DB 325 LDLTREPOLBEREOSQVAHGTNGIHVTGSMITGNITLYNGPVLGGPBGDLPATPBP 384
OY 333 P-ASTHLCTPGPASTHLCTPVQK 355
DB 333 P-ASTHLCTPGPASTHLCTPVQK 355
OY 385 PYPPEEGDPPPG---ISTPHQE 405
DB 385 PYPPEEGDPPPG---ISTPHQE 405

```

RESULT 6  
 GORUN  
 nerve growth factor receptor precursor, low affinity (validated) - human  
 N:Alternate names: NGF receptor  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 08-Dec-2000  
 C:Accession: A25218; A60204; S21699; I57638  
 R:Johnson, D.; Lananhan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.;  
 Cell 47, 545-554, 1986  
 A:Title: Expression and structure of the human NGF receptor.  
 A:Reference number: A25218; MUID:87051725; PMID:3022937  
 A:Accession: A25218  
 A:Molecule type: mRNA



A:Residues: 1-427 <JCH>  
A:Cross-references: GB:M14764; NID:G189204; PIDN:AA859544.1; PID:G189205  
R:Marano, N.; Diezschold, B.; Barley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;  
J. Neurochem. 48, 225-232, 1987  
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor  
A:Reference number: A60204; MUID:87085574; PMID:3025363  
A:Accession: A60204  
A:Molecule type: protein  
A:Residues: 29-31, 'T', '33-42', 'T', '45-46', 'TX', '50-51', 'XX', '54-56' <MAR>  
A:Experimental source: melanoma cell line A875  
A>Note: This sequence has been corrected by a note added in proof to follow the nucleot  
R:Vasavajjala, P.; Leszyk, J.D.; Lin-Gorke, J.; Ross, A.H.  
Arch. Biochem. Biophys. 294, 244-252, 1992  
A:Title: Structural domains of the extracellular domain of human nerve growth factor rec  
A:Reference number: S21689; MUID:92198017; PMID:1372492  
A:Accession: S21689  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 183-208 <VTS>  
R:Sehgal, A.; Patil, N.; Chao, M.  
Mol. Cell. Biol. 8, 3160-3167, 1988  
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor  
A:Reference number: 157638; MUID:89096903; PMID:2850481  
A:Accession: 157638  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-22 <RES>  
A:Cross-references: GB:M21621; NID:G189206; PIDN:AA836363.1; PID:G189207  
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C:Comment: This protein is thought to form a high-affinity receptor when it associates w  
C:Genetics:  
A:Gene: GDB:NGFR  
A:Cross-references: GDB:120234; OMIM:162010  
A:Map position: 17q21.17q22  
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-427/Product: nerve growth factor receptor #status experimental <MAT>  
F:32-250/Domain: extracellular #status predicted <EXT>  
F:32-65/Domain: NGF receptor repeat homology <NG1>  
F:67-108/Domain: NGF receptor repeat homology <NG2>  
F:109-147/Domain: NGF receptor repeat homology <NG3>  
F:149-189/Domain: NGF receptor repeat homology <NG4>  
F:197-248/Region: NGF receptor repeat homology <NG4>  
F:251-273/Domain: transmembrane #status predicted <TM>  
F:273-427/Domain: intracellular #status predicted <INT>  
F:60/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 9.1%; Score 236; DB 1; Length 427;  
Best Local Similarity 22.9%; Pred. No. 2,1e-07;  
Matches 111; Conservative 62; Mismatches 194; Indels 118; Gaps 22;

7 PGLLPVLPALLADVAGVGLVPHGDLKREKSPQCKYKHPONSTICCTCKHGT 66  
13 PRLILLILGLSLGAKA-----PPTGLYTH---SGECKKCNIGB 51  
67 YLYNDPCRGKRDTCRVAPG--TYTALNHLRCLSCRCDEMGOVLSPCVNDRTVC 125  
52 GVAOPC--GANOTVCEPLDVSFSDVVSATPECKPCTECVG--LQSNAPCEVADAVC 107  
126 GCRKNQYREYNGETFRCLNGLSPNGT-VNIPCOERDITC-HGKMFLLKAK-----C 179  
108 RC---AYGYQDETTGRCBACVCEAGGLVFSQDKNTVCBEPDGTYSDEAHNVDP 164  
180 ISCHDK-----NKECKLCPTR-----PSTGKSDPPTGTVLLPLVIVFG 220  
165 LPCTVCEPTEROLRECTRWADAECEH--FGKWTSTPPEGSDSTAPSTOE--PEAPPEQ 221  
221 LCASFASVILACRGKMKPKLSTIICGOSTLVKSGBEPLVAPAGFNPPTTICSSNPS 280  
222 DLIASTVAGVY-----TWGSSQPVVTTGTDDNLPLV-----YCSILA 260

QY 281 SSPVSIIPYI-----SCDRNFGAVASPSSEKAP-----HKAGDILGPPASTHLCT 329  
261 AVYVGLAVIAPFKRMNSCKQNKQGANRPVNGPPEPGEKHLHDSG--ISVDSGLHDOQ 318  
330 FGPPASTHLCTPPGPASTHLCTPVQKWEASAPAPDQADAPATLYAVVDGVPSPWKE 389  
319 PHQTASGALKGGGGLYSLPLPAKREVE-----KLINGSGADTWRH 361  
QY 390 LVRRILGS--SHEIERLENGRHLREAOYMLAARRRTPREATELLGRVLRDMDLG 448  
362 LAGSLGTQPEH-----IDSFTHACVRYALLMSW--AIQDSATLUALAALRRIQRAD 412  
QY 449 CLENI 453  
413 LVESL 417

RESULT 7  
A26431  
Nerve growth factor receptor precursor, low affinity - rat  
N:Alternate names: NGF receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
A:Accession: A26431; PH1229  
R:Radeke, M.J.; Misko, T.P.; Hau, C.; Herzenberg, L.A.; Shopler, E.M.  
Nature 325, 593-597, 1987  
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.  
A:Reference number: A26431; MUID:87115859; PMID:3027580  
A:Accession: A26431  
A:Molecule type: mRNA  
A:Residues: 1-425 <RAD>  
A:Cross-references: GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756  
R:Merz, M.; Timusk, T.; Allikmeets, R.; Saarma, M.; Persson, H.  
Gene 121, 247-254, 1992  
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoic  
A:Reference number: PH1229; MUID:93077038; PMID:11446821  
A:Accession: PH1229  
A:Molecule type: DNA  
A:Residues: 1-20 <MET>  
A:Cross-references: GB:X61269  
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C:Comment: This protein is thought to form a high-affinity receptor when it associates w  
C:Genetics:  
A:Introns: 20/3  
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-425/Product: nerve growth factor receptor #status predicted <MAT>  
F:33-66/Domain: extracellular #status predicted <EXT>  
F:68-109/Domain: NGF receptor repeat homology <NG1>  
F:110-148/Domain: NGF receptor repeat homology <NG2>  
F:150-190/Domain: NGF receptor repeat homology <NG3>  
F:198-249/Region: NGF receptor repeat homology <NG4>  
F:251-273/Domain: transmembrane #status predicted <TM>  
F:274-425/Domain: intracellular #status predicted <INT>  
F:61/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 8.7%; Score 227.5; DB 1; Length 425;  
Best Local Similarity 23.4%; Pred. No. 6.8e-07;  
Matches 107; Conservative 59; Mismatches 169; Indels 123; Gaps 24;

44 CPQCKYKHPONSTICCTCKHGTLYNDPCRGKRDTCRVAPG--TYTALNHLRCLSC 102  
33 CSTGLYTH---SGECKKCNIGBVAOPC--GANOTVCEPLDVSFSDVVSATPECKPC 87  
QY 103 SRCDEMFOVEISPCVNDRTVCRCRNQYREYNGETFRCLNGLSPNGT-VNIPCOER 161  
DB 88 TECIG--LQSNAPCEVADAVCAGVYOD--EFG-HCEACSVCEVSGLVFSQDK 142  
QY 162 QDTIC-HGKMFLLKAK-----CISCHDKKKECKLCPTRPSTGKSDP-PGTVLLPL 215

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Db      143 QNTVEBCEGEGYSDSBNVDPCLPCTVEDTE-RQLRRECTWMADECEITG----- 194
Qy      216 VVFGCLCLASFPASVVLACRYQRMKPKLYSIICGOSTLVKEGEDEL----LVPAQFNPT 270
Db      195 -----RWIPRSTPEGSDSSTAPSTOPEVEPEPDLPSTVADWV 233
Qy      271 TTICFSSSTP-----SSSPVSIIPYI-----SCDRNPGAVASPSSE 306
Db      234 TTVMSSSQGVVTRGTTDNILIPVCSLLAVVGLVAVYIAFKMNSCKQKQGANRPVNOQ 293
Qy      307 TAPP-----HLKAGPILPGPPASTHLCTPGPPASTHLCTPPGPA-----STHLCTPVQKW 356
Db      294 TPPEGEKIHSDG--ISVDSQSLH-----DQGHHTQASGQALKGDGNLVSSLPLTKR 345
Qy      357 EMSASAPDQGLADADPATIYAVDGVPSRMKELYRRLGLS-EHEIERLELENGHLEBA 415
Db      346 E-----EVERKLNIGD-----TWRHLAGELGQYDEH-----IDSFTHACP 380
Qy      416 QYSMLAAMRRRTPRREATLELGRVLRMDLGCLENI 453
Db      381 VRALLASWCAQD---SATIDALLALRLRGRADYIESL 415

```

## RESULT 8

```

JN0006
Nerve growth factor receptor, low affinity precursor - chicken
N.Alternate names: NGF receptor
C.Species: Gallus gallus (chicken)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: JN0006; A60504
R.Larage, T.H.; Weiskamp, G.; Helder, J.C.; Raadeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid
Neuron 2, 1123-1134, 1989
A.Title: Structure and developmental expression of the nerve growth factor receptor in t
A.Reference number: JN0006; MUID:90166579; PMID:2560385
A.Accession: JN0006
A.Molecule type: mRNA
A.Residues: 1-416 <LAR>
A.Experimental source: embryonic chick brain
R.Heuer, J.G.; Falcami-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A.Title: Structure and developmental expression of the chicken NGF receptor.
A.Reference number: A60504; MUID:90152140; PMID:2154393
A.Accession: A60504
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 21-35, 'Y', 37-172, 'K', 174-215, 'S', 277-395, 'R', 397-416 <HEU>
C.Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C.Comment: The cytosolic-rich region of the extracellular domain may form part or all of
C.Comment: This protein is thought to form a high-affinity receptor when it associates w
C.Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C.Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F.1-20/Domain: signal sequence #status predicted <SIG>
F.21-416/Product: nerve growth factor receptor #status predicted <MNT>
F.21-239/Domain: extracellular #status predicted <EXT>
F.24-57/Domain: NGF receptor repeat homology <NG1>
F.59-100/Domain: NGF receptor repeat homology <NG2>
F.101-139/Domain: NGF receptor repeat homology <NG3>
F.141-181/Domain: NGF receptor repeat homology <NG4>
F.189-237/Region: serine/threonine-rich
F.240-261/Domain: transmembrane #status predicted <MEM>
F.262-416/Domain: intracellular #status predicted <INT>
F.52/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match 8.5%; Score 220; DB 1; Length 416;

Best Local Similarity 23.3%; Pred. No. 1.9e-06;

Matches 116; Conservative 46; Mismatches 168; Indels 168; Gaps 25;

Qy 6 VPGLLPLVLALADVVRAGVQGLVPHRGDLEKRESPPQAGKYNNHFNQNSTICTCKHGK 65

Db 5 VRLLLLL-----PAG-----PTWGSKEK-----CLTKMT---TSECCCKACNLG 42

Qy 66 TYLVNDGPGRDIDRCVCAFG-TYTALENHLRLCLSCRCRDENFOVEISPCVVRDVT 124

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Db      43 EGVQPC--GVNOYVCEPCLDSVTSYSDTVASTBPCKPCTQCVG--LHSMAPCVESDVA 98
Qy      125 QGCRKNQRYREYMGTEGFRCLNCSLCPNG-TVINPCOERODTIC-HCHMGFLKGAK---- 178
Db      99 CRC--AVGYQDELSSGCKECSICEVQFGMLPFCRDSQDTVCEBCEPGTSDANFVDP 155
Qy      179 CISCHDK-----NKECEKLCR-----TRPSTCKSDODPT-----T 210
Db      156 CLPCTICEENVMWKECTASTDAECRDLHPRTWTHITSLASDSBEPITRDPFTGMAAT 215
Qy      211 VLLPLVIFGLCLASFPASVVLACRYQRMKPKLYSIICGOSTLVKEGEDELVPAQFNPT 270
Db      216 TLADIIV-----TWMSGQGVVTRGTTDNILIPV----- 243
Qy      271 TTICFSSSTPSSPVSIIPYI-----SCDRNPGAVASPSSETAP-----HLKAGPILP 319
Db      244 ---YCSLLAVVGLVAVYIAFKMNSCKQKQGANRPVNOQTSPEGEKIHSDGISVD 299
Qy      320 GPAPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKKEASAPADQGLADPATIYAVV 379
Db      300 ---SQSLHQDQPPNQS---TQGP-----APKGDGLVA-- 326
Qy      380 DGVPPSR-----WKELVRLGLSEHEIERLELENGHLEBAQYMLAAMR 424
Db      327 -SLPPSKQEBVEKLLSSAERTWQLAGELQYKEDLIDCFIRE-----ESPARALLADW- 379
Qy      425 RRTPRREATLELGRVLR 442
Db      380 --SAKETATIDALLVALR 395

```

## RESULT 9

```

JC7705
death receptor-6 - chicken
C.Species: Gallus gallus (chicken)
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C.Accession: JC7705
R.Bridgman, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A.Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A.Reference number: JC7705; MUID:21308433; PMID:11414698
A.Accession: JC7705
A.Molecule type: mRNA
A.Residues: 1-651 <BRI>
A.Cross-references: GB:AP349908
C.Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
C.Comment: to the TNF receptor superfamily, and is involved in cell death and/or survival signaling cascade.
C.Genetics:
A.Gene: dr-6
C.Keywords: ovary
F.1-21/Domain: signal sequence #status predicted <SIG>
F.52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F.332-350/Domain: transmembrane #status predicted <TM>
F.410-475/Domain: death domain #status predicted <DED>
F.551-651/Region: conserved cytoplasmic #status predicted

```

Query Match 7.7%; Score 199.5; DB 2; Length 651;

Best Local Similarity 22.9%; Pred. No. 5.3e-05;

Matches 125; Conservative 57; Mismatches 217; Indels 147; Gaps 30;

Qy 10 LPLPLVPLAL-----ADVVRAGVQGLVPHRGDLEKRESPPQAGKYNNHFNQNSTICTCK 62

Db 5 VLAVALPLVFLGRTADNORPLTS-----EQNAVSLPAGKTYLHIDRATNDELICDKC 55

Qy 63 HKGTLYVNDGPGRDT--DRCVCAFGTYTALENHLRLCLSCSR-CRDENFOVEISPCVV 119

Db 56 PACTYVSKHCT---KSTLRKCSPPCDGTFTKHENGIERCHCRKRPC--ELPMIEKTHCTA 110

Qy 120 DRDTVQSCRKQRYREYMGTEGFRCLNCSLCPNG-TVINPCOERODTIC-HCHMGF---- 173

Db 111 LTDECTCLSGTF-----QINDTCVPTVPCVGVGRKKTETEDVRCRKLPGTSDVP 165

QY 174 LKAKCTISCHDC-KN-----KECEKLC-----PTREPTGKSDODPCTYLLPLVI 217  
 Db 166 SSVAKCKCTYDDCFCKNNVVVVPKTESDNVCKSPASIPNTSLTSSDAQDETEAPEPTA 225  
 QY 218 VFGICLSPASVVLACRYQKPKLYSLICGQSTLVYEGEBELLVPAKGFPTTICPSS 277  
 Db 226 YLPKGLNS-----SVFDLSSSPARVSNGTAE-----PTVDIND 259  
 QY 278 TPSSSPVSIPIPYISCDRSNFGAVAS-----PSSETPAPHLKAGPILP--GP 321  
 Db 260 TSANGTGTAGPQSLLS-SAGTGAQOASYNHKTNSQAMKQPAEMAGKESSTIPYPRRGP 318  
 QY 322 P-ASTHLCTGPPAPSTHL-----CTPGPAPSTHLCTPVOKEMASAPSA 363  
 Db 319 PNWHQHF-----DINEHLPMWIVLFLVLVVIWVCSVRKSSRT-----LKKGRPROPSPA 368  
 QY 364 PDGLADADPAT-----LYAV-----VDGVPP-----SRMEELVRL--GLSEHEER 403  
 Db 369 IVEPAIKKSTTPPQNRKMYLYCNGHGDILKPVAAQVGSQWQDIYQFLCNASEREV-- 426  
 QY 404 LELENGRHL-REAOYSMLAARRRTPREATLELGRVLRMDLGLCTENIEALGCAAR 462  
 Db 427 AAFNGVAAADHRAVYALQHTIRGP--EASLAQLISALRGRNDVYEKIRGLMEDTTP 484  
 QY 463 LASEPR 468  
 Db 485 VOMQPO 490

## RESULT 10

A35356  
 tumor necrosis factor receptor 2 precursor [validated] - human  
 N/Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
 C/Species: Homo sapiens (man)  
 C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 08-Dec-2000  
 C/Accession: A35356; A36475; A48416; A36007; A23666; B55010; I38094  
 R/Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K  
 Science 248, 1019-1023, 1990  
 A/Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
 A/Reference number: A35356; MUID:90260639; PMID:2160731  
 A/Accession: A35356  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-461 <SMI>  
 A/Cross-references: GB:M23315; NID:G189185; PIDN:AAA59929.1; PID:G189186  
 R/Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; Kang, M.W.; Hale, K.K.; Squires,  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
 A/Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
 A/Reference number: A36475; MUID:91045991; PMID:2172983  
 A/Accession: A36475  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-195, 'R', 197-461 <KOH>  
 A/Cross-references: GB:M55994; GB:M38549; NID:G339757; PIDN:AAA36755.1; PID:G339758  
 R/Dembel, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.  
 Cytokine 2, 231-237, 1990  
 A/Title: Two human TNF receptors have similar extracellular, but distinct intracellular,  
 A/Reference number: A48416; MUID:91370690; PMID:1966549  
 A/Accession: A48416  
 A/Status: preliminary  
 A/Molecule type: mRNA, protein  
 A/Residues: 23-461 <DM>  
 A/Cross-references: GB:S63368; NID:G235648; PIDN:AA19824.1; PID:G235649  
 A/Note: Sequence extracted from NCBI backbone (NCBIN:63368, NCBIIP:63371)  
 R/Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
 A/Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra  
 A/Reference number: A36007; MUID:90349572; PMID:2166946  
 A/Accession: A36007  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
 A/Cross-references: GB:M55857; NID:G339751; PIDN:AAA63262.1; PID:G339752

R/Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.  
 J. Biol. Chem. 265, 20131-20138, 1990  
 A/Title: Purification and partial amino acid sequence analysis of two distinct tumor necr  
 A/Reference number: A23666; MUID:91056048; PMID:2173696  
 A/Accession: A23666  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 23-40;65-69;136-141;300-306 <LOE>  
 R/Engelmann, H.; Novick, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A/Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence f  
 A/Reference number: A35010; MUID:90110215; PMID:2153136  
 A/Accession: B35010  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 27-31 <ENG>  
 R/Kuhnert, P.; Kemper, O.; Wallach, D.  
 Gene 150, 381-386, 1994  
 A/Title: Cloning, sequencing and partial functional characterization of the 5' region of  
 A/Reference number: I38094; MUID:95121934; PMID:7821811  
 A/Accession: I38094  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-37 <RES>  
 A/Cross-references: EMBL:X80021; NID:G666044; PIDN:CAA56324.1; PID:G825701  
 A/Genes: GDB:TNFR2  
 A/Cross-references: GDB:125914; OMIM:191191  
 A/Map position: 1p36.2-1p36.2  
 A/Introns: 26/3  
 A/Note: the list of introns is incomplete  
 C/Suprafamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C/Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F/1-22/Domain: signal sequence #status predicted <SIG>  
 F/23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
 F/40-76/Domain: NGF receptor repeat homology <NG1>  
 F/78-119/Domain: NGF receptor repeat homology <NG2>  
 F/120-162/Domain: NGF receptor repeat homology <NG3>  
 F/164-201/Domain: NGF receptor repeat homology <NG4>  
 F/262-279/Domain: transmembrane #status predicted <TMN>  
 F/280-461/Domain: intracellular #status predicted <INT>  
 F/171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

## RESULT 11

Query Match 7.6%; Score 199; DB 1; Length 461;  
 Best Local Similarity 25.3%; Pred. No. 4.1e-05;  
 Matches 77; Conservative 26; Mismatches 103; Indels 98; Gaps 14;  
 QY 32 PHRPDLKREBPPCGQKKNPQNTICTCKHKTLYLNDGPGRPDPCVCAFGTYTA 91  
 Db 34 PEPG-----STCRLERY-YDQTAQMCCKSCSPQAHKVFCTKTS-DIVCSCSDSTYTQ 85  
 QY 92 LFNHLRCLSC-SRCRDEMFOVEISPCVDRDTVCGCRKNQYRYRWGTYGFRCLNCSLC- 149  
 Db 86 LMWVPECLSCGSCSSD--QVETQACTREQNRKICTCRPGYCALSKQEG-----CRCLA 138  
 QY 150 -----PNGVTNIPQERQDPTICHMGFLKAKKICSHDCKNKECKLCPTSPSTGKD 203  
 Db 139 PLKRCRPFQVABRGTETSDVVC-----KPCA----- 165  
 QY 204 SQDPGTVLPLVIVFGICLSPASVVLACRYQKPKLYSLICGQSTLVYEGEBELLVP 263  
 Db 166 ---PGT-----FSNTTSTDICPHQ-----ICN-----VVA 189  
 QY 264 AFGNPTTTCFSSSTPSS-----PVSIPPYISCDRSNFGAVASPSSETPAPHLKAGPILP 319  
 Db 190 IFGANSMDAVCTISPTKSMAPGAVHLPQPVSTSTSHQTPPERS--TAPSTSLPLRNGP 247  
 QY 320 GPPA 323  
 Db 248 SPPA 251

A42086  
 CD30 antigen precursor - human  
 N:Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jul-2000  
 C:Accession: A42086  
 R:Durkop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.  
 Cell 68, 421-427, 1992  
 A:Title: Molecular cloning and expression of a new member of the nerve growth factor rec  
 A:Reference number: A42086; MUID:92154659; PMID:1310894  
 A:Accession: A42086  
 A:Molecule type: mRNA  
 A:Residues: 1-595 <DUR>  
 A:Cross-references: GB:M83554; NID:9180095; PIDN:AAA51947.1; PID:9180096  
 A:Experimental source: HUT-102 cell line  
 A:Notes: Sequence extracted from NCBI backbone (NCBIN:82088, NCBI:82090)  
 C:Genetics:  
 A:Gene: GDB:CD30; DIS166  
 A:Cross-references: GDB:131547; OMIM:153243  
 A:Map position: 1p36-1p36  
 C:Superfamily: NGF receptor repeat homology  
 C:Keywords: glycoprotein; growth factor receptor; transmembrane protein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-383/Domain: extracellular #status predicted <EXT>  
 F:384-407/Domain: transmembrane #status predicted <TM>  
 F:408-595/Domain: intracellular #status predicted <CYT>  
 F:101,276/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.4%; Score 193; DB 2; Length 595;  
 Best Local Similarity 24.6%; Pred. No. 0.0012;  
 Matches 101; Conservative 42; Mismatches 166; Indels 102; Gaps 24;

Oy 41 ESPCQGVNHPQNTI--CCTKCHKGYLVNDGCPRPDPCR-VCAFGTYTALENLR 97  
 Db 26 EDTC-HGAPSHYDAVRCCTCRPMGLPTQC--PGRPTDCKQCEPDYLL--DEAD 79  
 Oy 98 RCLSCSRC-RDEMFQVEISPCVVDRTVCGCRKNQRYWYG-ETGFRCLNCSLCPNG-TV 154  
 Db 80 RCTACVTCSDRL--VEKTPCAMNNSRYCECRPMGFCSTANVSCARCFPHSVCAQMTIV 137  
 Oy 155 NIPCEBDDTICH-CHMFPFLKGAACISCHDCKNEC-----EKLCPTRPST----- 200  
 Db 138 KPFGTAKNTVCEPASPV---SPACASPENCKEPPSSGTTPOAKPTPVSPATSSATMPV 194  
 Oy 201 -----GKDSQDPETVLLVLVIFGLCLASFPASVLAARYQ 236  
 Db 195 RGTRLAQAASKLTRADPSVSGRPSSDPGLSTPQCPREGSDC-----RK 242  
 Oy 237 RWKPKLYSIICQGST-LVKEGPELLVPAP-GFNPTT-----ICFSSTPSSSPVSI 287  
 Db 243 QCEPDYVDEAGRCACVSCGRDLVEKTPCAMNNSRYCECRPMGICATSNASCARCV- 301  
 Oy 288 PYICSDRNFQAVASPSSETAPPHL-KAGPILPGPPASTHL-CTPGP-----PASTHLCT 340  
 Db 302 PYPIC-----AAETVTKQDAEKDTTFEAPRLCTOPDCNTPNNGRAPAST----- 348  
 Oy 341 PGPPASTHLCTPVQKWEASAPAPQDLADADPATLVAVVDGVPSPRMKELY 391  
 Db 349 -SPQSLVDSQASKTLPTFSAPVALS-----STGKPLVDAGPVLFWILV 394

RESULT 12  
 JC2395  
 Fas antigen precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Nov-1999  
 C:Accession: JC2395; PC2246  
 R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.  
 Biochem. Biophys. Res. Commun. 198, 666-674, 1994  
 A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat live  
 A:Reference number: JC2395; MUID:94128114; PMID:7507668  
 A:Accession: JC2395  
 A:Molecule type: mRNA

A:Residues: 1-324 <KIT>  
 A:Cross-references: DBJ:D26112; NID:9468486; PIDN:BA05108.1; PID:d1005650; PID:9468487  
 A:Experimental source: thymus  
 A:Accession: PC2246  
 A:Molecule type: mRNA  
 A:Residues: 1-62, 'RFT' <KIT>  
 A:Cross-references: DBJ:D26113; NID:9468488; PIDN:BA05109.1; PID:d1005651; PID:9468489  
 A:Experimental source: liver  
 C:Genetics:  
 A:introns: 62/1  
 C:Superfamily: NGF receptor repeat homology  
 C:Keywords: transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-324/Product: Fas antigen #status predicted <MAT>  
 F:44-79/Domain: NGF receptor repeat homology <NGF>  
 F:81-124/Domain: NGF receptor repeat homology <NG4>  
 F:171-188/Domain: transmembrane #status predicted <TM>

Query Match 7.0%; Score 181.5; DB 2; Length 324;  
 Best Local Similarity 23.5%; Pred. No. 0.00034;  
 Matches 71; Conservative 39; Mismatches 107; Indels 85; Gaps 13;

Oy 10 LPLVLPALLADVYPAGVQGL---VPHGDLKRESPQCKYNNHPNSTICCTKCHKGT 66  
 Db 7 VLPLVLAGPELVNMGCDISIFEGLELKRSYRETDNCSBGLY---QVGPCCOCPGCG 63  
 Oy 67 YLVNDCPQGRDTCRVCAFG-TYTALENHLRCLSCSRCDMEFQVEI-SPCVDRDPTV 124  
 Db 64 RKVDDCTTSGAPFCHPCTEBGEYTRKHVSDKRCRCAFC-DEHGGLVEFTNCRTOGTK 122  
 Oy 125 CGCRKNQRYREWGTGFRCLNCSLCPNQTIVIPQEBODTICHMGMFPLGACISCHD 184  
 Db 123 CRCKENFY-----CNASLCDH-----CYHCTS 144  
 Oy 185 CKNKECEKLCPTRPSTGKDSQDPETVLLPLVIFGLCLASFPASVLAARYQWKPKLYS 244  
 Db 145 CGLBDILPCC-TRISNTRCKKQSSNYKLWLLILPGLAI---LVFYIKRYRKQP----- 196  
 Oy 245 IICQSTLVKEGPELLVPAGFPPTTTCRSPSS-SPVSIPTPYI-----SCDRS 295  
 Db 197 -----GDPESGISP-----ESVPMVSDVNLKMYTRTAKMKICPAK 235  
 Oy 296 NF 297  
 Db 236 KF 237

RESULT 13  
 B43692  
 T2 protein - rabbit fibroma virus  
 C:Species: rabbit fibroma virus, Shope fibroma virus  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: B43692  
 R:Upton, C.; Delange, A.M.; McFadden, G.  
 Virology 160, 20-30, 1987  
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric  
 A:Reference number: A43692; MUID:87321103; PMID:2820128  
 A:Accession: B43692  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-325 <UPT>  
 A:Cross-references: GB:M17433  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
 F:64-105/Domain: NGF receptor repeat homology <NG2>  
 F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 7.0%; Score 181.5; DB 2; Length 325;  
 Best Local Similarity 29.6%; Pred. No. 0.00034;  
 Matches 58; Conservative 16; Mismatches 81; Indels 41; Gaps 12;

Oy 14 VLPLALADVYPAGVQGLVPHGDLKRESPQCKYNNHPNSTICCTKCHKGYLVNDCP 73  
 Db 4 LIALLVCVVYVYGD--VPY-----SSNQGCKGCHDY---EKDGLCCASCHGPFVASRLC- 53

QY 74 GPGADTDRCVCAFGTYTALLENHARRCLSC-SRCDREMFQVEISPCVVDRTVCGCRKNQY 132  
 DB 54 GPGSITVSPCEDGFTASTHAPACVSCRGCTGHL--SESQPCDRTHDRVCNCSSTGNY 111  
 QY 133 REYMGCTFRCLNCSLNGTNTVPCQERQDPTICHCHNGFPLKAKCTSCHD-CNKKECE 191  
 DB 112 CLKKGNG-----CRICAPQT-----KCPAGVGS-----HTRADDTLCE 147  
 QY 192 KLCEPTPSTGKDSQDP 207  
 DB 148 K-CP--PHTYSDSLSP 160

## RESULT 14

QVZML  
 T2 protein - myxoma virus (strain Lausanne)

C/Species: myxoma virus  
 C/Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999  
 C/Accession: A40566  
 R/Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.  
 Virolology 184, 370-382, 1991  
 A/Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor  
 A/Reference number: A40566; MUID:91335768; PMID:1651597  
 A/Accession: A40566  
 A/Molecule type: DNA  
 A/Residues: 1-326 <UP>  
 A/Cross-references: GB:M5181; GB:M37976; NID:9332309; PID:AAA6632.1; PID:9332310  
 C/Suprafamily: myxoma virus T2 protein; NGF receptor repeat homology  
 C/Keywords: glycoprotein  
 F/64-105/Domain: NGF receptor repeat homology <NG2>  
 F/106-147/Domain: NGF receptor repeat homology <NG3>  
 F/166-181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.9%; Score 180; DB 1; Length 326;  
 Best Local Similarity 35.5%; Pred. No. 0.00042;

Matches 50; Conservative 11; Mismatches 64; Indels 16; Gaps 7;

QY 14 VLPALLADVPAVGVLVPHRDLEKRESPPQCKYNNHNPONSTICCTCKHKGTYLYNDCP 73  
 DB 6 LLAAVVAACVYGGG-----APYGADRGK-----CRGNVY---EKDGLCTSCPPGSAVSRNC- 53  
 QY 74 GPGADTDRCVCAFGTYTALLENHARRCLSC-SRCDREMFQVEISPCVVDRTVCGCRKNQY 132  
 DB 54 GPGSITVSPCEDGFTASTHAPACVSCRGCTGHL--SESQPCDRTHDRVCNCSSTGNY 111  
 QY 133 REYMGCTFR-CLNCSLCPNG 152  
 DB 112 CLKKGNGCRICAPKTKCPAG 132

## RESULT 15

B38634  
 tumor necrosis factor receptor type 2 precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999

C/Accession: B38634; A40254; S54816

R/Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A/Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor  
 A/Reference number: A38634; MUID:91187885; PMID:1849278

A/Accession: B38634

A/Molecule type: mRNA

A/Cross-references: GB:M60469; NID:9199827; PID:AAA9752.1; PID:9199828

R/Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk  
 Mol. Cell. Biol. 11, 3020-3026, 1991

A/Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
 A/Reference number: A40254; MUID:91246168; PMID:1645445

A/Accession: A40254

A/Molecule type: mRNA

A/Residues: 1-474 <GO>

A/Cross-references: GB:M60469; NID:9199827; PID:AAA9752.1; PID:9199828

R/Kisomergis, M.; Fellows, R.; Feldmann, M.; Chernaiova, Y.  
 submitted to the EMBL Data Library, May 1995

A/Description: Characterization of the promoter region of the murine p75-TNF receptor.

A/Reference number: S54816

A/Accession: S54816

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-22 <KIS>

A/Cross-references: EMBL:X87128; NID:9809043; PID:CAA60618.1; PID:9809044

C/Suprafamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

C/Keywords: cytokine receptor; transmembrane protein

F/1-22/Domain: signal sequence; #status predicted <SIG>

F/23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>

F/40-77/Domain: NGF receptor repeat homology <NG1>

F/79-120/Domain: NGF receptor repeat homology <NG2>

F/166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 6.9%; Score 178.5; DB 2; Length 474;  
 Best Local Similarity 23.1%; Pred. No. 0.00075;  
 Matches 80; Conservative 36; Mismatches 138; Indels 93; Gaps 16;  
 QY 32 PHPDLEKRESPPQCKYNNHNPONSTICCTCKHKGTYLYNDCRGDRDRCVCAFGTYTA 91  
 DB 34 PEPG-----YECISQSYIDRAKQWCCAKCPQGVYVHFC-NKTSPTVCADCEASMTQ 86  
 QY 92 LENHARRCLSC-SRCDREMFQVEISPCVVDRTVCGCRKNQYREYMGCTGF--RCLNCSL 148  
 DB 87 VMNQFRTCLSSSSCTTD--QVEIRACTKQNNRCACAEAGRYCALKTHSSGRCRCOMLSK 144  
 QY 149 C-----PNTVYNIPQERQDPTICHCHNGFPLKAKCTSCHDCKNKEKLCPT 197  
 DB 145 CGPFGVAASSRAPNGNV-----LC-----KAC--A 167  
 QY 198 PSTGKDSQDPETVLLPLVIVFGCLASPAVAVLACRYGRKPKLYSICQSTLVVEGE 257  
 DB 168 PGTSDTTS-STDCRPHRISILAIPOANSTDAVCAPE--SPTLSAI--PRTLYVSOPE 222  
 QY 258 PEL-----LVPAQFNPTTTCFSSTP-----SSPVSIPPIYISCDRSNFG-----A 299  
 DB 223 PTRSQPLDQBERGPGQTSILTSLSSTPIIBSTGCGSLPIGLVGVTSGLMLGLVNC 282  
 QY 300 VASPSSETAPPHLKAGPILPEPP-----ASTHLCTPGPPAST 336  
 DB 283 IILVQRKKKPSCLORDAKVPHVPEKSDQDAVGLRQHLTLTAPSSSS 329

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 Job time : 22 secs

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OM protein - protein search, using sw model

Run on: September 13, 2003, 06:56:04 ; Search time 17 Seconds

(without alignments)  
1302.916 Million cell updates/sec

Title: US-09-970-532-2

Perfect score: 2603  
Sequence: 1 MGLPTVPGLLPLVLPALLA.....NIEFALGGAARLASEPRLLW 471

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_A1.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2603	100.0	471 1	TR1A_BOVIN
2	1750	67.2	461 1	TR1A_PIG
3	1517	58.3	455 1	TR1A_HUMAN
4	1338.5	51.4	461 1	TR1A_RAT
5	1319	50.7	454 1	TR1A_MOUSE
6	387.5	14.9	417 1	TR25_HUMAN
7	271.5	10.4	440 1	TR10B_HUMAN
8	257	9.9	435 1	TRR3_HUMAN
9	247	9.5	415 1	TRR3_MOUSE
10	236	9.1	427 1	TR16_HUMAN
11	227.5	8.7	425 1	TR16_RAT
12	221.5	8.5	417 1	TR16_MOUSE
13	220	8.5	416 1	TR16_CHICK
14	199	7.6	461 1	TR1B_HUMAN
15	196	7.5	176 1	TR23_MOUSE
16	195	7.5	655 1	TR21_HUMAN
17	195	7.5	655 1	TR21_MOUSE
18	194.5	7.5	180 1	TR22_MOUSE
19	193	7.4	595 1	TRR8_HUMAN
20	191.5	7.4	381 1	TR10B_MOUSE
21	185	7.1	468 1	TRR6_RAT
22	181.5	7.0	324 1	TRR6_MOUSE
23	181.5	7.0	325 1	TRR6_PIG
24	180	6.9	326 1	TRR6_BOVIN
25	178.5	6.9	474 1	TRR6_MOUSE
26	171.5	6.6	259 1	TRR6_HUMAN
27	171.5	6.6	283 1	TRR6_MOUSE
28	169	6.5	3718 1	TRR6_MOUSE
29	168.5	6.5	289 1	TRR6_MOUSE
30	167	6.4	332 1	TRR6_PIG
31	167	6.4	323 1	TRR6_MOUSE
32	166	6.4	351 1	TRR6_BOVIN
33	166	6.4	401 1	TRR6_MOUSE

34	163.5	6.3	349 1	CRMB_CAMPS
35	163.5	6.3	349 1	CRMB_VARV
36	162	6.2	327 1	TRR6_HUMAN
37	161	6.2	327 1	TRR6_MOUSE
38	160.5	6.2	300 1	TRR6_HUMAN
39	160.5	6.2	1696 1	PKCS_BRACL
40	160	6.1	401 1	TR1B_MOUSE
41	158	6.1	824 1	AD08_HUMAN
42	155.5	6.0	269 1	TRR5_BOVIN
43	155	6.0	1877 1	PKCS_MOUSE
44	154	5.9	870 1	SRC2_HUMAN
45	153.5	5.9	625 1	TR11_MOUSE

## ALIGNMENTS

RESULT 1

ID	TR1A_BOVIN	STANDARD	PRG	471 AA
AC	019131;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)			
DN	(TNF-R1) (TNF-R1) (p55).			
GN	TNFRSF1A OR TNFR1.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Arteria;			
RX	MEDLINE=96273505; PubMed=9613449;			
RA	Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;			
RT	"Cloning and sequencing of cDNA encoding bovine tumor necrosis factor			
RT	(TNF)-receptor I.";			
RL	Ver. Immunol. Immunopathol. 61:379-385(1998).			
CC	-1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric			
CC	TNFSF1/Lymphotoxin-alpha. The adaptor molecule FADD recruits			
CC	caspase-8 to the activated receptor. The resulting death-inducing			
CC	signaling complex (DISC) performs caspase-8 proteolytic activation			
CC	which initiates the subsequent cascade of caspases (apoptate-)			
CC	specific cysteine proteases) mediating apoptosis (By similarity).			
CC	-1- SUBUNIT: Binding of TNF to the extracellular domain leads to			
CC	homotrimerization. The aggregated death domains provide a novel			
CC	molecular interface that interacts specifically with the death			
CC	domain of TRADD. Various TRADD-interacting proteins such as TRAFs,			
CC	RIP and possibly FADD, are recruited to the complex by their			
CC	association with TRADD. This complex activates at least two			
CC	distinct signaling cascades, apoptosis and NF-kappa-B signaling.			
CC	Binds Bcl2 (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type 1 membrane protein.			
CC	-1- SIMILARITY: Contains 4 TNFR-Cys repeats.			
CC	-1- SIMILARITY: Contains 1 death domain.			
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.ebi.ac.uk/announce/">http://www.ebi.ac.uk/announce/</a>			
CC	or send an email to <a href="mailto:license@ebi.ac.uk">license@ebi.ac.uk</a> ).			
CC	EMBL; U90937; AA65143.1; -			
CC	HSSP; P19438; 1TRR.			
CC	InterPro; IPR000488; Death.			
CC	InterPro; IPR001368; TNFR_C6.			
CC	Pfam; PF00531; death.1.			
CC	Pfam; PF00020; TNFR_C6; 3.			
CC	SMART; SM00005; DEATH; 1.			

DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 471  
 FT DOMAIN 22 210  
 FT TRANSMEM 211 233  
 FT DOMAIN 234 471  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 195  
 FT DOMAIN 340 360  
 FT DOMAIN 360 360  
 FT DOMAIN 372 457  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 194  
 FT DISULFID 185 190  
 FT CAROAMD 54 54  
 FT CAROAMD 145 145  
 FT CAROAMD 151 151  
 SO SEQUENCE 471 AA; 51367 MW; 5243EF514DF8B1C4 CRC64;

Query Match 100.0%; Score 2603; DB 1; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 4,36-159;  
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLPVPGLLLPLVLPALLADYVPAVGQVGVPHPGDLEERESPCCQGYKYNHONSTICT 60  
 DB 1 MGLPVPGLLLPLVLPALLADYVPAVGQVGVPHPGDLEERESPCCQGYKYNHONSTICT 60  
 QY 61 KCHKSTLYNDPCPGRDYDCVCAFGTYTALENHARRCLSCGRDEMFOVEISPCVVD 120  
 DB 61 KCHKSTLYNDPCPGRDYDCVCAFGTYTALENHARRCLSCGRDEMFOVEISPCVVD 120  
 QY 121 RDTVCGCKNOYREYWGEGFRCNLCSLCPNGTVNI PCQERODTI CHCHMGFPLKAGCTI 180  
 DB 121 RDTVCGCKNOYREYWGEGFRCNLCSLCPNGTVNI PCQERODTI CHCHMGFPLKAGCTI 180  
 QY 181 SCHDKNKECEKLCPTPSTGKSDPGTTLVPLVIVFGCLASFASVVLACRYQWKP 240  
 DB 181 SCHDKNKECEKLCPTPSTGKSDPGTTLVPLVIVFGCLASFASVVLACRYQWKP 240  
 QY 241 KLYSIICQSTLYVKEGEPELLVPAGFNPPTTICFSSSTPSSSPVSIPIYISCDSNFGAV 300  
 DB 241 KLYSIICQSTLYVKEGEPELLVPAGFNPPTTICFSSSTPSSSPVSIPIYISCDSNFGAV 300  
 QY 301 ASPSETAPPHLKAPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLCCTPVQWMSA 360  
 DB 301 ASPSETAPPHLKAPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLCCTPVQWMSA 360  
 QY 361 PSAPQCLADADPATLYAVVDGVPSPRMKELVRRLGLSHEHETRELENGRHLEAEOYML 420  
 DB 361 PSAPQCLADADPATLYAVVDGVPSPRMKELVRRLGLSHEHETRELENGRHLEAEOYML 420  
 QY 421 AAMRRRTRENTATLELGRVLRMDLGLCLENIEEALGGAARLASERPILW 471  
 DB 421 AAMRRRTRENTATLELGRVLRMDLGLCLENIEEALGGAARLASERPILW 471

RESULT 2  
 TRIA\_PIG

ID TRIA\_PIG STANDARD; PRT: 461 AA.  
 AC PS0555;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R1) (p55).  
 GN TNFRSF1A OR TNFR1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteleostomi; Cetartiodactyla; Suidae; Sus.  
 OX NCBI\_Taxid=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=96011645; PubMed=7590278;  
 RA Suter B., Pauli U.H.;  
 RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor";  
 RU Gene 163:263-266(1995).  
 CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (apartate-specific cysteine proteases) mediating apoptosis (By similarity).  
 CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to homotrimerization. The aggregated death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various TRADD-interacting proteins such as TRAFs, RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
 CC Blinds BAC4 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
 CC -----  
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 CC -----  
 DR EMBL; U19994; AAC48499.1; -.  
 DR PIR; JC4302; JC4302.  
 DR HSRP; P19438; TNFR.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 461  
 FT DOMAIN 22 210  
 FT TRANSMEM 211 233  
 FT DOMAIN 234 461  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 195  
 FT DOMAIN 340 350  
 FT DOMAIN 350 447  
 FT DISULFID 44 58  
 FT DISULFID 59 72





RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywiecki M.I., Skalska U., Smalhus D.E.,  
 RA Schercher A., Schein J.E., Jones S.J.W., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [9]  
 RP SEQUENCE OF 41-45.  
 RX MEDLINE=90110215; PubMed=2153136;  
 RA Engelmann H., Novitsky D., Wallach D.,  
 RT "Two tumor necrosis factor-binding proteins purified from human  
 RT urine. Evidence for immunological cross-reactivity with cell surface  
 RT tumor necrosis factor receptors.";  
 RL J. Biol. Chem. 265:1531-1536 (1990).  
 RN [10]  
 RP INTERACTION WITH BAG4.  
 RX MEDLINE=99115917; PubMed=9915703;  
 RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.,  
 RT "Prevention of constitutive TNF receptor 1 signaling by silencer of  
 RT death domains.";  
 RL Science 283:543-546 (1999).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.  
 RX MEDLINE=93258809; PubMed=8387891;  
 RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,  
 RA Broger C., Leitescher H., Lesslauer W.,  
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
 RT beta complex: implications for TNF receptor activation.";  
 RL Cell 73:431-445 (1993).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 RX MEDLINE=97094982; PubMed=8939750;  
 RA Nalemlth J.H., Devine T.O., Khono H., Sprang S.R.,  
 RT "Structure of the extracellular domain of the type I tumor necrosis  
 RT factor receptor.";  
 RL Structure 4:1251-1262 (1996).  
 RN [13]  
 RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.  
 RX MEDLINE=99213501; PubMed=10199409;  
 RA McDermott M.F., Aksenitjevich I., Galon J., McDermott E.M.,  
 RA Ogunkolade B.W., Centola M., Mansfield E., Gadiña M., Karanko L.,  
 RA Peterson T., McCarty J., Frucht D.M., Aringer M., Torosyan Y.,  
 RA Teppo A.-M., Wilson M., Karaatman H.M., Wan Y., Todd I., Wood G.,  
 RA Schlimen R., Kumarajewa T.R., Cooper S.M., Vella J.P., Ames C.I.,  
 RA Mulvey J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J.,  
 RA Hittman G.A., O'Shea J., Kaestner D.L.,  
 RT "Germline mutations in the extracellular domains of the 55 kDa TNF  
 RT receptor, TNFR1, define a family of dominantly inherited  
 RT autoinflammatory syndromes.";  
 RL Cell 97:133-144 (1999).  
 RN [14]  
 RP FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis. Contributes to  
 CC the induction of noncytotoxic TNF effects including anti-viral  
 CC state and activation of the acid sphingomyelinase.  
 CC -1 SUBUNIT: Binding of TNF to the extracellular domain leads to  
 CC homotrimerization. The aggregated death domains provide a novel  
 CC molecular interface that interacts specifically with the death  
 CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
 CC RIP and possibly FADD, are recruited to the complex by their  
 CC association with TRADD. This complex activates at least two  
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
 CC BINDS BAG4.  
 CC SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
 CC -1 DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO  
 CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH  
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
 CC -1 PM: The soluble form is produced from the membrane form by  
 CC proteolytic processing.  
 CC -1 DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant

CC familial hibernian fever (FHF), a disease characterized by  
 CC recurrent fever, abdominal pain, localized tender skin lesions and  
 CC myalgia.  
 CC -1 SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1 SIMILARITY: Contains 1 death domain.  
 CC -1 DATABASE: NAME=PROV; NOTE=CD guide CD120a entry;  
 CC MMW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".  
 CC -----  
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 CC -----  
 CC DR EMBL; X55313; CAAB9021.1; -;  
 CC DR EMBL; M33294; AAA03210.1; -;  
 CC DR EMBL; M58286; AAA36753.1; -;  
 CC DR EMBL; M63121; AAA36754.1; -;  
 CC DR EMBL; M75866; AAA61201.1; -;  
 CC DR EMBL; M75864; AAA61201.1; JOINED.  
 CC DR EMBL; M75865; AAA61201.1; JOINED.  
 CC DR EMBL; M60275; AAA36756.1; -;  
 CC DR EMBL; A21522; CAAB1558.1; -;  
 CC DR EMBL; A131997; AAM77802.1; -;  
 CC DR EMBL; BC010140; AAM77802.1; -;  
 CC DR PIR; A38208; GQH071.  
 CC DR PDB; 1TNR; 31-JUL-94.  
 CC DR PDB; 1NCF; 07-DEC-95.  
 CC DR PDB; 1EXT; 11-JAN-97.  
 CC DR PDB; 1FT4; 12-OCT-01.  
 CC DR PDB; 1ICH; 01-APR-02.  
 CC DR GeneW; HGNC:11916; TNFRSF1A.  
 CC DR MIM; 191190; -;  
 CC DR GO; GO:0005576; C:extracellular; TAS.  
 CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC DR GO; GO:0005032; P:tumor necrosis factor receptor, type I acti. . .; TAS.  
 CC DR GO; GO:0007165; P:signal transduction; TAS.  
 CC -----  
 CC Query Match 58.3%; Score 1517; DB 1; Length 455;  
 CC Best Local Similarity 62.9%; Pred. No. 6.8e-90;  
 CC Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;  
 CC -----  
 CC QY 1 MGLPTVPCLLPLVLPALADVYPAGVOGLVPHPGDLEKRSPPQCKYHNPONSTICT 60  
 CC DB 1 MGLSTVPDLPLPLVLELVLWGIYPSVIGLVPHLGDRKRSVCPQCKYIHPONNSICT 60  
 CC QY 61 KCHGTYLYNDCPGPRGRTDCRCVAPGTYTALENHLRRCISCSRCRDEMPQVEISPCVVD 120  
 CC DB 61 KCHKTYLYNDCPGPGQDTRCEBSSGFTASBNHLRCLSCSKCKRMGOVEIISCTVD 120  
 CC QY 121 RDTVCGCKNRYRYWGEYGTGRFCLNCSICPGNTVNIPOQERDPTICCHMGFFPKGAKCI 180  
 CC DB 121 RDTVCGCKNRYRYWSENLECFNCSICLNGTVHLSQGEKQNTVCTCHAGFPLRENECV 180  
 CC QY 121 RDTVCGCKNRYRYWSENLECFNCSICLNGTVHLSQGEKQNTVCTCHAGFPLRENECV 180  
 CC DB 121 RDTVCGCKNRYRYWSENLECFNCSICLNGTVHLSQGEKQNTVCTCHAGFPLRENECV 180  
 CC QY 181 SCHCKRK-EERKICPTRPSTGKSDOPGTVLLPLVIVELGLCLASPSAVYLACRYQWK 239  
 CC DB 181 SCHCKRK-EERKICPTRPSTGKSDOPGTVLLPLVIVELGLCLASPSAVYLACRYQWK 239  
 CC QY 181 SCSSCKKSLKCTKCLPDIENVKGTEDSGTVLLPLVIFGLCLSLFGLIMRYQWK 240  
 CC DB 181 SCSSCKKSLKCTKCLPDIENVKGTEDSGTVLLPLVIFGLCLSLFGLIMRYQWK 240  
 CC QY 240 PKLVIICGOSTLVKEGPE-----LVVAPGFNP-----TTICFSSPTSSSPVSIPIYI 290  
 CC DB 240 PKLVIICGOSTLVKEGPE-----LVVAPGFNP-----TTICFSSPTSSSPVSIPIYI 290  
 CC QY 241 SKLVIYCGKSTPEKEGELBETTKPLAPNPSFPTPEFTTLGFSVPSSSTFTSSRYT 300  
 CC DB 241 SKLVIYCGKSTPEKEGELBETTKPLAPNPSFPTPEFTTLGFSVPSSSTFTSSRYT 300  
 CC QY 291 SCDSNFGAVASPSESTAPPLKAGPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLC 350  
 CC DB 291 SCDSNFGAVASPSESTAPPLKAGPILPGPPASTHLCCTGPPASTHLCCTGPPASTHLC 350  
 CC QY 301 PGDCPNF---AAPREVAPPYGADPIL-----ATL-----ASDPIP 335  
 CC DB 301 PGDCPNF---AAPREVAPPYGADPIL-----ATL-----ASDPIP 335  
 CC QY 351 TPVQKWEASASAPDQADADPATLVAVVGVGVPSPKWEIVLRIGLSHEIERLENGR 410  
 CC DB 351 TPVQKWEASASAPDQADADPATLVAVVGVGVPSPKWEIVLRIGLSHEIERLENGR 410  
 CC QY 336 NPLQKWEASA-HKQPSLDTPDPAVLVAVENVVPLRWKEFVRRLGLSDHEIDRLQNGR 394  
 CC DB 336 NPLQKWEASA-HKQPSLDTPDPAVLVAVENVVPLRWKEFVRRLGLSDHEIDRLQNGR 394

QY 411 HREAQVSLAMRRRTPREATLELGRVLPDMMLGCTENIERALGGAARLASEPRLL 470  
 DB 395 CUREQVSLMTWRRRTPREATLELGRVLPDMMLGCTENIERALGGAARLASEPRLL 454

RESULT 4  
 ID TRIA RAT STANDARD; PRT; 461 AA.  
 AC P22934; Q91V30; Q91Y93;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R1) (p55).  
 OS TNFRSF1A OR TNFR1 OR TNFR-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=91090841; PubMed=1702293;  
 RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,  
 RA Lantcz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;  
 RT "Molecular cloning and expression of human and rat tumor necrosis  
 RT factor receptor chain (p60) and its soluble derivative, tumor  
 RT necrosis factor-binding protein.";  
 RL DNA Cell Biol. 9:705-715(1990).  
 [2]  
 RN SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.  
 RC STRAIN=BB1DR/Mor, LEW/NHsd, ACI/Seghnd, DA/Bkl, F344/NHsd, and  
 RC BN/SMNSd;  
 RA Furuya T., Salstrom J.L., Bina J., Hashiramoto A., Dobbins D.E.,  
 RA Wilder R.L., Remmers E.F.;  
 RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus  
 RT among autoimmune susceptible and resistant inbred rat strains.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF1/lymphotxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis (by similarity).  
 CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to  
 CC homotrimerization. The aggregated death domains provide a novel  
 CC molecular interface that interacts specifically with the death  
 CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
 CC RIP and possibly FADD, are recruited to the complex by their  
 CC association with TRADD. This complex activates at least two  
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.

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CC EMBL; M63122; AAA42256.1; -  
 DR EMBL; AF329976; AAK53562.1; -  
 DR EMBL; AF329977; AAK53563.1; -  
 DR EMBL; AF329981; AAK53567.1; -  
 DR EMBL; AF329978; AAK53564.1; -  
 DR EMBL; AF329979; AAK53565.1; -  
 DR EMBL; AF329980; AAK53566.1; -  
 DR PIR; B36555; GORP11.  
 DR HSP; P19438; INCF.  
 DR InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00520; TNFR\_c6; 4.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH DOMAIN; 1.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 461  
 FT  
 FT DOMAIN 22 211  
 FT TRANSMEM 212 234  
 FT DOMAIN 235 461  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 344 354  
 FT DOMAIN 363 448  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
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 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 195  
 FT CARBOHYD 185 191  
 FT CARBOHYD 54 54  
 FT CARBOHYD 151 151  
 FT CARBOHYD 201 201  
 FT VARIANT 230 230  
 FT VARIANT 295 295  
 SO SEQUENCE .461 AA; 50966 MW; 50969 MD; EB230545FBDD202 CRC64;

Query Match 51.4%; Score 1338.5; DB 1; Length 461;  
 Best Local Similarity 55.8%; Pred. No. 1.6e-78;  
 Matches 269; Conservative 51; Mismatches 114; Indels 47; Gaps 9;

QY 1 MGPIPTVGLLPVLPALLADVTYPAQVGLVPHPGDLERKSPQCKYHNPONSTICT 60  
 DB 1 MGLPIVPGLLSLVLLALMGHPSGVTLVPSLGDREKRDNLCPQKYAHPRNNSICT 60

QY 61 KCHKGTVLVNDGPGPRDTCRCVACPGTVTALENHRLRCISCRCDENVQVETISPCVD 120  
 DB 61 KCHKGTVLVSDCSPGQETVCEVCDKGTFTASGNHVRQCISCTCKRKEVQVETISPCAD 120

QY 121 RDTVCGCRKNQYREYNGETGFRCLNCSLCPNGTVNTPCOERDPTICGHWGFLAKAKI 180  
 DB 121 MDTVCGCKKQKQFQRYLSETHPQCVDSPCNGTVITPCREKQTVTCNCHAGFLSNECT 180

QY 181 SCHDC-KNKECEKLCPTPSTGKOSDPTTVLLPLVIVFGCLASFAVVLACRQWRK 239  
 DB 181 PCHCKKNQDECMKLCPPVAVNVTNPQDSGTAVALPLVIFGLCLLPFCISLTCRYPQR 240

QY 240 PKLYSIICGSGTLVKGGEPLV-----PAGGFNT-----TTICSSTPSS 282  
 DB 241 PRVYSIICRDSAVKVEGEIVTKPLTPASIPASPNNGFNPLGFTTPRSHVVSST 300

QY 283 PVSIPIYISCDRNSFGAVASPSSETAPPHLKAGPILPGEPASTHLCPTGPASTHLCPTG 342  
 DB 301 PIS-PVF-----GPSNMENFVPPVREVVPTQ-GADPILYGS-----LNFV 338

QY 343 P-PASTHLCPTPVQKWAASAPADQADPATVLAIVVDGPPSRKELVRRIGLSEHEI 401  
 DB 339 PIPA-----PVAKWEDVVAADQFORLDTADPMLVAVVDGVPPTRWKEFMRLLGLSEHEI 392

402 ERLEIENGHRHREAOYSMLAMRRRTTREPRTLELGRVLDMDLGLLENIEEALGGA 461  
 DB 393 ERLEIENGHRHREAOYSMLAMRRRTTREPRTLELGRVLDMDLGLLENIEEALGGA 452  
 RESULT 5  
 TRIA\_MOUSE STANDARD; PRT; 454 AA.  
 ID TRIA\_MOUSE  
 AC P25118;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R1) (p55).  
 GN TNFRSF1A OR TNFR1 OR TNFR-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RX MEDLINE=9118785; PubMed=1849278;  
 RA Lewis M., Taragaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 Wong G.H., Chen E.Y., Goeddel D.V.;  
 "Cloning and expression of cDNAs for two distinct murine tumor  
 necrosis factor receptors demonstrate one receptor is species  
 specific."  
 Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerry R., Davis T., Brannan C.I.,  
 Copeland N.G., Jenkins N.A., Smith C.A.;  
 "Molecular cloning and expression of the type 1 and type 2 murine  
 receptors for tumor necrosis factor."  
 Mol. Cell. Biol. 11:3020-3026(1991).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91285014; PubMed=1647956;  
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissoneghia A.M.,  
 Gray P.W., Feldmann M., Foxwell B.M.J.;  
 "Cloning, expression and cross-linking analysis of the murine p55  
 tumor necrosis factor receptor."  
 Eur. J. Immunol. 21:1649-1656(1991).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92039815; PubMed=1657766;  
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;  
 "Molecular cloning and expression of the mouse Tnf receptor type b."  
 Immunogenetics 34:338-340(1991).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94425292; PubMed=8188324;  
 RA Bebo B.P., Linthicum D.S.;  
 "Nucleotide sequence of the TNF type I receptor from a mouse  
 endotheloma cell line."  
 Immunogenetics 39:450-451(1994).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93156721; PubMed=831516;  
 RA Rothe J., Bluthmann H., Gentz R., Lesslauer W., Steinmetz M.;  
 "Genomic organization and promoter function of the murine tumor  
 necrosis factor receptor beta gene."  
 Mol. Immunol. 30:165-175(1993).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Krauseberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stempilton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Ustin T.B., Toshiyuki S., Cantucci P., Sprexer C.,  
 Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Heillon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 Schercher A., Schein J.B., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences."  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Receptor for TNFRSF2/TNF-alpha and homotrimeric  
 TNFRSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 caspase-8 to the activated receptor. The resulting death-inducing  
 signaling complex (DISC) performs caspase-8 proteolytic activation  
 which initiates the subsequent cascade of caspases (aspartate-  
 specific cysteine proteases) mediating apoptosis (By similarity).  
 CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to  
 homotrimerization. The aggregated death domains provide a novel  
 molecular interface that interacts specifically with the death  
 domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
 RIP and possibly FADD, are recruited to the complex by their  
 association with TRADD. This complex activates at least two  
 distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
 CC Binds BAG4 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 DR EMBL; M60468; AAA39751.1; .  
 DR EMBL; M59377; AAA40464.1; .  
 DR EMBL; X59238; CAA41922.1; .  
 DR EMBL; X57796; CAA40936.1; .  
 DR EMBL; L26349; AAA39361.1; .  
 DR EMBL; M76656; AAA40465.1; .  
 DR EMBL; M88067; AAA40465.1; JOINED.  
 DR EMBL; M76655; AAA40465.1; JOINED.  
 DR EMBL; BC004599; AAH04599.1; .  
 DR PIR; A38634; GQWST1.  
 DR HSSP; P19438; IEXT.  
 DR MGD; MGI:1314884; Tnfrsf1a.  
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.  
 DR GO; GO:0006952; P:defense response; IMP.  
 DR GO; GO:0006954; P:inflammatory response; IMP.  
 DR GO; GO:0007515; P:lymph gland development; IMP.  
 DR InterPro; IPR000486; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR SMART; SMO0005; DEATH; 1.  
 DR SMART; SMO0208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH DOMAIN; 1.  
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 454  
 FT DOMAIN 22 212  
 FT TRANSMEM 213 235  
 FT POTENTIAL.  
 FT TUMOR NECROSIS FACTOR RECEPTOR  
 FT SUPERFAMILY MEMBER 1A.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.

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FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 196 TNFR-CYS 4.
FT DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 356 441 DEATH.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 195 BY SIMILARITY.
FT DISULFID 185 191 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 394 394 R -> G (IN REF. 6).
SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 50.7%; Score 1319; DB 1; Length 454;
Best Local Similarity 56.5%; Pred. No. 2,8e-77;
Matches 268; Conservative 55; Mismatches 109; Indels 42; Gaps 12;

OY 1 MGELPTVGGLLPLVLPALADVPAGVGLVPHRGDLEKRSPPGCKYHNPQSTICT 60
DB 1 MGELPTVGGLLPLVLPALADVPAGVGLVPHRGDLEKRSPPGCKYHNPQSTICT 60
OY KCHKGTVLYNDPCPGRDTCRCVAPGYTALNHLRLRCLSCSCSRDMPFVETISPCVD 120
DB KCHKGTVLYNDPCPGRDTCRCVAPGYTALNHLRLRCLSCSCSRDMPFVETISPCVD 120
OY 61 KCHKGTVLYNDPCPGRDTCRCVAPGYTALNHLRLRCLSCSCSRDMPFVETISPCVD 120
DB 61 KCHKGTVLYNDPCPGRDTCRCVAPGYTALNHLRLRCLSCSCSRDMPFVETISPCVD 120
OY 121 RDVTCGRKQRYREYWGEGTFRCLNCSLCPNGYVNIPOQERODTCHGCMGFPAKACI 180
DB 121 RDVTCGRKQRYREYWGEGTFRCLNCSLCPNGYVNIPOQERODTCHGCMGFPAKACI 180
OY 121 KDTVCGCGKENGOFQYVLTSTHFCVDCSPCFNGVTYIPEKFTONTVCNCHAGFPLRESBCV 180
DB 121 KDTVCGCGKENGOFQYVLTSTHFCVDCSPCFNGVTYIPEKFTONTVCNCHAGFPLRESBCV 180
OY 181 SCHNC-KKKECEKIC-PRPSTGKSDQDPGTUPLPLVTVGLCLASPAVVALCRYORW 238
DB 181 SCHNC-KKKECEKIC-PRPSTGKSDQDPGTUPLPLVTVGLCLASPAVVALCRYORW 238
OY 181 PCHCKCKNEBCKMLCLPPPLANNVTNPOSGTAVLLPLVLLGLCLSLFISLMCRYPRW 240
DB 181 PCHCKCKNEBCKMLCLPPPLANNVTNPOSGTAVLLPLVLLGLCLSLFISLMCRYPRW 240
OY 239 KPKLYSIICGOSTVYK--GEPELLVAPGFNPPT--TICFSSTPSSSPVSIPIYIS 291
DB 239 KPKLYSIICGOSTVYK--GEPELLVAPGFNPPT--TICFSSTPSSSPVSIPIYIS 291
OY 241 RPEVYSITCRDPVYVKEKAKGFLTPASPAFSPISGPNFTLGSTPFGSSPVSTP--- 297
DB 241 RPEVYSITCRDPVYVKEKAKGFLTPASPAFSPISGPNFTLGSTPFGSSPVSTP--- 297
OY 292 CDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCPTG--PPASTHLCPTGPPASTH 348
DB 292 CDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCPTG--PPASTHLCPTGPPASTH 348
OY 298 -----ISPIFGPSNM-----HFM-----PVSSEVPFGQADPLLYESLCVPAF----- 336
DB 298 -----ISPIFGPSNM-----HFM-----PVSSEVPFGQADPLLYESLCVPAF----- 336
OY 349 LCTPVQKWEAA--SSAPQLADADPATLYAVVQGVPEKRWELVRRGLSHEHETLE 407
DB 349 LCTPVQKWEAA--SSAPQLADADPATLYAVVQGVPEKRWELVRRGLSHEHETLE 407
OY 337 --TSVQKEDSAHPORPD--NADLALIVAVVDGPPARWKEFPMFMSHEIEREMO 391
DB 337 --TSVQKEDSAHPORPD--NADLALIVAVVDGPPARWKEFPMFMSHEIEREMO 391
OY 408 NGRHLREAOYMLAAMRRTPRREATEELGRVLDMDLLCLENIEEALGAA 461
DB 408 NGRHLREAOYMLAAMRRTPRREATEELGRVLDMDLLCLENIEEALGAA 461
OY 392 NGRCLREAOYMLAAMRRTPRREATEELGRVLDMDLLCLENIEEALGAA 445
DB 392 NGRCLREAOYMLAAMRRTPRREATEELGRVLDMDLLCLENIEEALGAA 445

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DE mediating receptor TRAMP (Death domain receptor 3) (WSL protein)
DE (Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated
DE receptor of death) (LARD).
GN TNFRSF25 OR TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.
RC TISSUE=Lymphoid;
RX MEDLINE=97088617; PubMed=8934525;
RA Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
RA Grinham C.J., Brown R., Farrow S.N.;
RT "A death-domain-containing receptor that mediates apoptosis.";
RL Nature 384:372-375(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Umbilical vein endothelial cells;
RX MEDLINE=97081063; PubMed=8875942;
RA Chinaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
RA Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
RT "Signal transduction by DR3, a death domain-containing receptor
RT related to TNFR-1 and CD95.";
RL Science 274:990-992(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Heart;
RX MEDLINE=97148200; PubMed=8994832;
RA Martens S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
RA Goddard A.D., Bauer K.D., Ashkenazi A.;
RT "Apo-3, a new member of the tumor necrosis factor receptor family,
RT containing a death domain and activates apoptosis and NF-kappa-B.";
RL Curr. Biol. 6:1669-1676(1996).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
RX MEDLINE=97272273; PubMed=9114039;
RA Screation G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
RX MEDLINE=98113360; PubMed=946802;
RA Matzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
RA Salles G.;
RT "A new death receptor 3 isoform: expression in human lymphoid cell
RT lines and non-Hodgkin's lymphomas.";
RL Biochem. Biophys. Res. Commun. 243:376-379(1998).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Hayashizawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,
RA Shiozawa S., Sato M., Shiozawa K., Tsukamoto Y.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 4-417 FROM N.A.
RC TISSUE=Brain, and Fetal Lung;
RX MEDLINE=97205335; PubMed=9052839;
RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
RA Thome M., Bornand T., Hahne M., Schroeder M., Wilson A., French L.E.,
RA Browning J.L., Macdonald H.R., Teichmann J.;
RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology
RT to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RL Immunity 6:79-88(1997).
RN [9]
RP SEQUENCE OF 7-417 FROM N.A.
RC TISSUE=Brain;
RA Chaudhary P.M., Hood L.E.;

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OY 352 PVQK-----EASAPADPOLADADA-----TLVAVDGPSPRMKELVR 393  
 DB 294 FQVWMSWDQPSRALGPAAAPLTPSPSPAGSPAMMOPPOLYDMDAVPAPRMKEFVRT 353  
 OY 394 LGLSHEIERLENGRHLREAOVSMLAMRRRTREARTELLGRVLDMDLGCLENI 453  
 DB 354 LGLREAELEAVEVEIGR-FRDOQYEMLRKROQP--AGLQAVYVALLERMGLDGCVEDL 409  
 OY 454 BEAL 457  
 DB 410 RSRL 413  
 RESULT 7  
 ID 1108 HUMAN STANDARD; PRT: 440 AA.  
 AC 014763; 014720; 015508; 015517; 015531; Q9BVE0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL receptor-2) (TRAIL-R2).  
 GN TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF N-TERMINUS.  
 RC TISSUE=Forebrain Fibroblast;  
 RX MEDLINE=97459925; PubMed=9311998;  
 RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y., Bojani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A., Goodwin R.G., Rauch C.T.;  
 RA "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";  
 RT EMO J. 16:5386-5397(1997).  
 RL [2]  
 RN SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND ALTERNATIVE SPLICING.  
 RP TISSUE=; MEDLINE=97431692; PubMed=9285725;  
 RX Screation G.R., Mongkolkeha J., Xu X.-N., Cowper A.E.,  
 RA Michael A., Bell J.I.;  
 RT "TRICK2, a new alternatively spliced receptor that transduces the cytotoxic signal from TRAIL.";  
 RL Curr. Biol. 7:693-696(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG), AND CHARACTERIZATION.  
 RC TISSUE=Liver, and Spleen; MEDLINE=9603016; PubMed=9373179;  
 RX Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N., Tschopp J.;  
 RA "Characterization of two receptors for TRAIL.";  
 RT FEBS Lett. 416:329-334(1997).  
 RL [4]  
 RN SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RP TISSUE=Ovary;  
 RX MEDLINE=97467719; PubMed=9326928;  
 RA Wu G.S., Burns T.F., McDonald B.R. III, Jiang W., Meng R., Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R., Spilner N.B., Markowitz S., Wu G., el-Deiry W.S.;  
 RA "Killer/DR5 is a DNA damage-inducible p53-regulated death receptor gene.";  
 RT Nat. Genet. 17:141-143(1997).  
 RL [5]  
 RN SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RX MEDLINE=97390508; PubMed=9242610;  
 RA Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;  
 RT "An antagonist decoy receptor and a death domain-containing receptor for TRAIL.";  
 RL Science 277:815-818(1997).  
 RL [6]

RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RX MEDLINE=97467318; PubMed=9325248;  
 RA MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T., Cohen G.M., Alnemri E.S.;  
 RT "Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL.";  
 RL J. Biol. Chem. 272:25417-25420(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RX MEDLINE=96090092; PubMed=9430227;  
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
 RT "Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 RL Immunity 7:821-830(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RX MEDLINE=97390509; PubMed=9242611;  
 RA Sheridan J.P., Masters S.A., Picti R.M., Gurney A., Skubatch M., Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I., Goddard A.D., Godowski P., Ashkenazi A.;  
 RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy receptors.";  
 RL Science 277:818-821(1997).  
 RN [9]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG).  
 RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;  
 RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2 gene in colorectal carcinoma.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RA Cao X., Zhang W., Wan T.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RA Farran T., Vu T., Gilbert T., Gross J., O'Hara P.;  
 RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG).  
 RC TISSUE=Cervix;  
 RX MEDLINE=22386257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins L., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Dietzenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.V., Scheetz T.E., Brownstein M.J., Ueda T.B., Tomihataki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E., Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.  
 RX MEDLINE=20017054; PubMed=10549288;  
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ullrich M., O'Connell M., Kelley R.F., Ashkenazi A., de Vos A.M.;  
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5.";  
 RL Mol. Cell 4:563-571(1999).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.  
 RX PubMed=10542098;

RA Mongkolkeha J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
 RA Jones E.Y., Sreeton G.R.;  
 RA "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.";  
 RL Nat. Struct. Biol. 6:1048-1053(1999).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The  
 CC adaptor molecule FADD recruits caspase-8 to the activated  
 CC receptor. The resulting death-inducing signaling complex (DISC)  
 CC performs caspase-8 proteolytic activation which initiates the  
 CC subsequent cascade of caspases (separate-specific cysteine  
 CC proteases) mediating apoptosis. Promotes the activation of NF-  
 CC kappaB.  
 CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Long; Synonym=TRICK2B;  
 CC IsoId=O14763-1; Sequence=Displayed;  
 CC Name=Short; Synonym=TRICK2A;  
 CC IsoId=O14763-2; Sequence=VSP\_006490;  
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;  
 CC very highly expressed in tumor cell lines such as HeLa S3, K562,  
 CC HL-60, SW480, A549 and G361; highly expressed in heart, peripheral  
 CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,  
 CC ovary, uterus, placenta, testis, esophagus, stomach and throughout  
 CC the intestinal tract; not detectable in brain.  
 CC -1- INDUCTION: TNFSF10B is regulated by the tumor suppressor p53.  
 CC -1- DISEASE: Defects in TNFSF10B may be a cause of squamous cell  
 CC carcinoma of the head and neck.  
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
 CC -----  
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 CC or send an email to [license@isb-eb.ch](mailto:license@isb-eb.ch)).  
 CC -----  
 DR EMBL, AF016849; AAC51778.1; -;  
 DR EMBL, AF018657; AAB70577.1; -;  
 DR EMBL, AF018658; AAB70578.1; -;  
 DR EMBL, AF016266; AAB81180.1; -;  
 DR EMBL, AF022386; AAB71949.1; -;  
 DR EMBL, AF026288; AAB67109.1; -;  
 DR EMBL, AF020501; AAB71412.1; -;  
 DR EMBL, AF016268; AAC01565.1; -;  
 DR EMBL, AF012535; AAB67103.1; -;  
 DR EMBL, AB014718; BAA33723.1; -;  
 DR EMBL, AB014710; BAA33723.1; JOINED.  
 DR EMBL, AB014711; BAA33723.1; JOINED.  
 DR EMBL, AB014712; BAA33723.1; JOINED.  
 DR EMBL, AB014713; BAA33723.1; JOINED.  
 DR EMBL, AB014714; BAA33723.1; JOINED.  
 DR EMBL, AB014715; BAA33723.1; JOINED.  
 DR EMBL, AB014716; BAA33723.1; JOINED.  
 DR EMBL, AB014717; BAA33723.1; JOINED.  
 DR EMBL, AF153687; AAF75587.1; -;  
 DR EMBL, AF192548; AAF07175.1; -;  
 DR EMBL, BC001281; AAH01281.1; -;  
 DR PDB, 1D0G; 22-OCT-99.  
 DR PDB, 1D4V; 01-NOV-99.  
 DR Genew, HGNC:11905; TNFSF10B.  
 DR MIM, 603612; -;  
 DR MIM, 601400; -;  
 DR GO, GO:0016021; C:integral to membrane; IC.  
 DR GO, GO:0016506; F:apoptosis activator activity; NAS.  
 DR GO, GO:0008656; F:caspase activator activity; NAS.  
 DR GO, GO:0004872; F:receptor activity; NAS.  
 Query Match 10.4%; Score 271.5; DB 1; Length 440;  
 Best Local Similarity 25.5%; Pred. No. 1.6e-10;

Matches 123; Conservative 57; Mismatches 196; Indels 107; Gaps 25;  
 QY 4 PTVGGLLPLVPLADLVPAAGVGLVPHRQDEKRSPPQCKKYNHPOKSTICTCH 63  
 DB 32 PRVPTLVVAALL--VSASALITQODLAPQQAAPQQRSSPSGL-----CP 82  
 QY 64 KGTLYNDPCPGRDTRCVCAPG-TYALENHLRCLSCRCRDENQVEISPCVDND 122  
 DB 83 PGHHISD---GR-DCISRYGQDYS THNNDLFLCRLRC--DSGEVLSPTTTRN 134  
 QY 123 TVCCGRKNQYREYWGEGFRCLNSL-CPNGTVNI-PCQERODTC-HCHMGFLKAKC 179  
 DB 135 TVCCCEBGTFR--EDSEPMCKRCRTGCPRMVYKGDCTPMSDIECVKESG----- 184  
 QY 180 ISCHDKKKECKLCPRPSTGKXSDPGTIVLPLVPLCLASFASV--VLACRYQR 237  
 DB 185 -TKISGEPAVEEVTSSPGT-----PASCSLSGII-GVTVAAVVLIAVFKSKLL 236  
 QY 238 WK---PKLYSIIICGSTLVKEGPELVPAAGFNPPTTICFSSPSSPVSIPIYISCDR 294  
 DB 237 WKYVLPIYKIGICSGSG-----GDEPRV-----DR 260  
 QY 295 SNFGAVASPSSETAPPHLKAPILPG--PPASTHLCPPGPPASTHLCPPGPPASTHLC 352  
 DB 261 SS---QPGABDVNLNIVSIILOPTQVPEQEMVEQEPAPPTGVNMLSPG--ESEHLLP 314  
 QY 353 VQKKKASAPSPDOLADNPA-TIYAVDS---VPERKVELVRLGLSHEIERLELE 407  
 DB 315 AEARSORRLLVPANEDPTETRQCFDPADLVPEDSWPLMKKGLMNEIKVAEAE 374  
 QY 408 NGRHLREAOYEMLAAMRRTPREATTLELGRVLRMDMLCLCLENIEBALGAARLASBP 467  
 DB 375 AAGH-ROTLTYMLIKMVKKT-----GRDASVHTLLALBTLSGRL--AKOKIED 420  
 QY 468 RLL 470  
 DB 421 HLL 423  
 RESULT 8  
 TRN3 HUMAN STANDARD; PRT; 435 AA.  
 AC P36941;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 3 precursor  
 DE (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related  
 DE protein) (Tumor necrosis factor C receptor).  
 DE LTR OR TNFRSF3 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93252381; PubMed=8486360;  
 RA Baens M., Chaffanet M., Casaman J.J., den Berghe H., Marynen P.;  
 RT "Construction and evaluation of a hncDNA library of human 12p  
 RT transcribed sequences derived from a somatic cell hybrid.";  
 RL Genomics 16:214-218(1993).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan G.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkings R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uadiri T.B., Toshitsuki S., Carninci P., Prange C.,



RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallue D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [3]  
 RP FUNCTION.  
 RX MEDLINE=94225209; PubMed=8171323;  
 RA Crowe P.D., VandeRade T.L., Walter B.N., Ware C.F., Hession C.,  
 RA Ehrenfele B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
 RT "A lymphotoxin-beta-specific receptor.";  
 RL Science 264:707-710(1994).  
 [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=9923511; PubMed=10207006;  
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;  
 RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell  
 RT death in HeLa cells.";  
 RL J. Biol. Chem. 274:11868-11873(1999).  
 [5]  
 RP FUNCTION.  
 RX MEDLINE=20261554; PubMed=10799510;  
 RA Rooney I.A., Butrovich K.D., Glaes A.A., Borboroglu S., Benedict C.A.,  
 RA Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;  
 RT "The lymphotoxin-beta receptor is necessary and sufficient for  
 RT LIGHT-mediated apoptosis of tumor cells.";  
 RL J. Biol. Chem. 275:14307-14315(2000).  
 [6]  
 RP INTERACTION WITH TRAF3.  
 RX MEDLINE=96278943; PubMed=8663299;  
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,  
 RA Yagita H., Okumura K.;  
 RT "TRAF3, an activator of NF-kappaB and putative signal transducer for  
 RT the lymphotoxin-beta receptor.";  
 RL J. Biol. Chem. 271:14661-14664(1996).  
 [7]  
 RP INTERACTION WITH TRAF4.  
 RX PubMed=9626059;  
 RA Krajewska M., Krajewski S., Zapata J.M., VandeRade T.,  
 RA Gascogne R.D., Berern K., McFadden D., Shadick A., Hugh J.,  
 RA Reynolds A., Cleverger C.V., Reed J.C.;  
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal  
 RT adult, fetal, and tumor tissues.";  
 RL Am. J. Pathol. 152:1549-1561(1998).  
 [8]  
 RP INTERACTION WITH TRAF5.  
 RX MEDLINE=98172745; PubMed=9511754;  
 RA Mizushima S.-I., Fujita M., Ichida T., Azuma S., Kato K., Hirai M.,  
 RA Otsuka M., Yamamoto T., Inoue Y.-I.;  
 RT "Cloning and characterization of a cDNA encoding the human homolog of  
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";  
 RL Gene 207:135-140(1998).  
 [9]  
 RP FUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
 CC LTA and LTB, and for TNF514/LIGHT. Promotes apoptosis via TRAF3  
 CC and TRAF5. May play a role in the development of lymphoid organs.  
 CC -1- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -----  
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 CC -----  
 DR EMBL: L04270; AAA36757.1;  
 DR EMBL: BC026262; AAH26262.1;  
 DR PIR: I54182; I54182.  
 DR HSSP: P25942; ICDP.  
 DR Genew: HGNC:6718; LTBR.  
 DR MIM: 600979;  
 DR GO: GO:0007165; P:signal transduction; TAS.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 4.  
 DR SMART: SM0208; TNFR; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS00050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 435  
 FT  
 FT DOMAIN 31 227  
 FT TRANSMEM 228 248  
 FT DOMAIN 249 435  
 FT REPEAT 42 81  
 FT REPEAT 82 124  
 FT REPEAT 125 168  
 FT REPEAT 169 211  
 FT DISULFID 43 58  
 FT DISULFID 59 72  
 FT DISULFID 62 80  
 FT DISULFID 83 98  
 FT DISULFID 101 116  
 FT DISULFID 104 124  
 FT DISULFID 126 132  
 FT DISULFID 139 148  
 FT DISULFID 142 167  
 FT DISULFID 170 185  
 FT CARBOHYD 40 40  
 FT CARBOHYD 177 177  
 SQ SEQUENCE 435 AA; 46709 MW; 624626B6022P656F CRC64;  
 Query Match 9.9%; Score 257; DB 1; Length 435;  
 Best local similarity 27.3%; Pred. No. 1,36-09;  
 Matches 121; Conservative 37; Mismatches 158; Indels 128; Gaps 25;  
 1 MGLP---TVPGILLV-PLVP--ALLADVPAGVGLVPHPGDEKRSPCKQKYNHPON 54  
 1 MLFPMASRGLANGPLVGLFGLLAASPOAV-PRASINQCRDQEKETYEBOH 55  
 55 STICTCKCHKGTLYLNDPCGGRDTRVCAFGTYTALENHLRCLSCSRCDMPQVEI 114  
 56 -RICSCRCPTGYVSAC-SRIRDTVCATCAENSYNHMNVLTICQCRPCDPVWGLEI 113  
 115 SPVCVDDYVCGCKKQYREWGRTGRCLNCSL---CPNCTVNIPOEROYDT----- 165  
 114 APTSKRKTQCRCPGMFCAM--ALECTHCCLSDCPPE-ALNDEVGKNNH 166  
 166 -CHCHMGFFLK---GAKTCSCHDCKKCEKCLCP---TRSTGKDSODP-----GT-- 209  
 167 CVPKAGHPONTSPSPARCQPHRCENQGLVEAPGTAOSDTTKNLEPILPPMSGTM 226  
 210 --TVLPLVIVFGCLASFASVVLACRYORWKPKLYGIIQGSTLVYEGEBELLVPAFG 267  
 227 MLAVLPL--AFPLLATVFSCL-----WKS--HPSLCKKGLSKLRROQ-----GSGP 271  
 268 NPTTTCFSSPTSPSPISIPY-----ISCDS--NFGVAVSPSSTAP----- 310  
 272 NPV-----AGSWEPKAPHYPPDLVQPLPLISGDVSPVSTGLPAAPVLEAGVPOOSP 324  
 311 -----HLKAGPILPAPPASTHL-CTPGP 332  
 325 LIDLREQLRBEBSQVAHGTNGHVTGSMITIGNIVTNGVPLGSPGPGDLPATPEP 384  
 333 P-ASTHLCTPGPASTHLCTPVOK 355

DB 385 PYPBEGDPPGPG--LSTPHQE 405

# RESULT 9

TNR3 MOUSE STANDARD; PRT; 415 AA.

ID TNR3 MOUSE

AC P50284;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 3 precursor

GN LTR OR TNFRSF3 OR TNFCR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI\_TaxID=10090;

OR NCI\_TaxID=10090;

RA SEQUENCE FROM N.A.

RA STRAIN=CVB; TISSUE=Lung;

RA MEDLINE=96072804; PubMed=7594541;

RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,

RA Browning J.L., Ware C.F.;

RA "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,

RA and expression.";

RL J. Immunol. 155:5280-5288(1995).

RL [2]

RA SEQUENCE FROM N.A.

RA MEDLINE=96163885; PubMed=8586432;

RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,

RA Horjo T.;

RA "The murine lymphotoxin-beta receptor cDNA: isolation by the signal

sequence trap and chromosomal mapping.";

RL Genomics 30:312-319(1995).

RL [3]

RA INTERACTION WITH TRAF5.

RA STRAIN=BALB/c;

RA MEDLINE=96278943; PubMed=8663299;

RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,

RA Yagita H., Okumura K.;

RA "TRAF5, an activator of NF-kappaB and putative signal transducer for

the lymphotoxin-beta receptor.";

RL J. Biol. Chem. 271:14661-14664(1996).

CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing

LTR and LTR, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3

and TRAF5. May play a role in the development of lymphoid organs

(By similarity).

CC -1- SUBUNIT: Self-associates (By similarity). Associates with TRAF3.

CC Associates with TRAF3 and TRAF4 (By similarity).

CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.

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DR EMBL; U29173; AAA68964.1; .

DR EMBL; U38423; AAB00846.1; .

DR EMBL; U30798; AAB81334.1; .

DR HSSP; O14763; 100G.

DR MCD; MG1104875; Ltblr.

DR InterPro; IPR001368; TNFR\_C6.

DR Pfam; PF00020; TNFR\_C6; 3.

DR SMART; SMO0208; TNFR\_3.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS00650; TNFR\_NGFR\_2; 3.

KM Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 30 POTENTIAL.

FT CHAIN 31 415 TUMOR NECROSIS FACTOR RECEPTOR

FT DOMAIN 31 223 SUPERFAMILY MEMBER 3.

FT TRANSMEM 224 244 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).

FT REPEAT 42 81 TNFR-CYS 1.

FT REPEAT 82 124 TNFR-CYS 2.

FT REPEAT 125 170 TNFR-CYS 3.

FT REPEAT 171 213 TNFR-CYS 4.

FT DISULFID 43 58 BY SIMILARITY.

FT DISULFID 59 72 BY SIMILARITY.

FT DISULFID 62 80 BY SIMILARITY.

FT DISULFID 83 98 BY SIMILARITY.

FT DISULFID 101 116 BY SIMILARITY.

FT DISULFID 104 124 BY SIMILARITY.

FT DISULFID 126 132 BY SIMILARITY.

FT DISULFID 139 150 BY SIMILARITY.

FT DISULFID 142 169 BY SIMILARITY.

FT DISULFID 172 187 BY SIMILARITY.

FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 415 AA; 44956 MM; 29B326A56AEF661 CRC64;

Query Match 9.5%; Score 247; DB 1; Length 415;

Best Local Similarity 25.8%; Pred. No. 5.5e-09;

Matches 105; Conservative 46; Mismatches 168; Indels 88; Gaps 20;

12 PLVPLALLADVPYAGVGLVPHPDLEKRESPCQKYNHONSTICTCKHKTLYLND 71

16 PLLLG--LSGLVLSQPLVP--PRIENQTCWDQKEYEPMHD--VCCSRCPGEFVAV 71

72 CPFGPDTCVCVAGTYTALENLRCLSCSRDEMFQVEISPCVDRDTVCGCRNQ 131

72 C-SNSQDTVCCTCHNSYNEHNMNLSCTCLRPDDIVLGFPEVAPCTSDRAEBCRCQGM 130

132 YREYWGTEGFRCLNCS---LCPNGTVINPCQERDITICH--CHMGFLK---GAKC 179

131 SCVLLDN---ECVACEERVLVCPGTEAEVTDIMDVAVCPCKRGHFGNTSSPRARC 187

180 ISCHDCKNKCEKLCPTRPSTG-----KDSQDGTLYLPLVVFGLCLASPAVYLAC 233

188 QPHTRC---ETQGLVEAAPGYSYSDTICKNPBEGAMLL--LAILLSVLFLFTYVLAC 242

234 RYQRMKPLXYSIICGO-STLVK---EGEPBLVAPGFNP-----TTTICFSSSTPSSP 283

243 AMNR-----HSLRKLKGLTKRHPGEESPPCAPADPHFPDLARLPLMSDLSFSP 297

284 VSIPT-----YISCDRNSPGAVASPS-----SETAPPHIKA 314

298 AGPTAPSLBERVLQOQSPVQARELEAPGEHGVHANGANGIVTGSVVTGNIYVN 357

315 GPLRG-----PPASTHLCTPGPASTHLCTPPASTHLCTPVOK 355

358 GPVLGTRGPGDPPA-----PPBPPTP--EBGAPPSLSTPYOE 397

RESULT 10

TR16 HUMAN STANDARD; PRT; 427 AA.

ID TR16 HUMAN

AC P08138;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-

affinity nerve growth factor receptor) (NGF receptor) (gp80-LNFR)

DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).

GN NGFR OR TNFRSF16.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

RA SEQUENCE FROM N.A.

RA MEDLINE=87051725; PubMed=3022937;

RA Johnson D., Lanahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,  
 RA Botwell M., Chao M.;  
 RT "Expression and structure of the human NGF receptor.";  
 RL Cell 47:545-554(1986).  
 RN (2)  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=89096903; PubMed=2850481;  
 RA Sehgal A., Patel N., Chao M.;  
 RT "A constitutive promoter directs expression of the nerve growth factor  
 RT receptor gene.";  
 RL Mol. Cell. Biol. 8:3160-3167(1988).  
 RN (3)  
 RP INTERACTION WITH TRAF2, TRAF4 AND TRAF6.  
 RX PubMed=10514511;  
 RA Ye X., Mehlen P., Rabinzadeh S., VanArsdale T., Zhang H., Shin H.,  
 RA Wang J.J., Leo E., Zapata J.M., Hauser C.A., Reed J.C., Bredesen D.E.;  
 RT "TRAF family proteins interact with the common neurotrophin receptor  
 RT and modulate apoptosis induction";  
 RL J. Biol. Chem. 274:30202-30208(1999).  
 RN (4)  
 RP INTERACTION WITH TRAF6.  
 RX PubMed=9915784;  
 RA Khursigara G., Orlinick J.R., Chao M.V.;  
 RT "Association of the p75 neurotrophin receptor with TRAF6.";  
 RL J. Biol. Chem. 274:2597-2600(1999).  
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,  
 CC and NT-4. Can mediate cell survival as well as cell death of  
 CC neural cells.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-  
 CC associated cell death executor. Interacts with TRAF2, TRAF4 and  
 CC TRAF6.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: N- AND O-glycosylated.  
 CC -1- PTM: Phosphorylated on serine residues.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
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FT REPEAT 148 188 TNFR-CYS 4.  
 FT DOMAIN 344 421 DEATH.  
 FT DOMAIN 197 248 SER/THR-RICH.  
 FT DISULFID 32 43 BY SIMILARITY.  
 FT DISULFID 44 57 BY SIMILARITY.  
 FT DISULFID 47 64 BY SIMILARITY.  
 FT DISULFID 67 83 BY SIMILARITY.  
 FT DISULFID 86 99 BY SIMILARITY.  
 FT DISULFID 89 102 BY SIMILARITY.  
 FT DISULFID 109 122 BY SIMILARITY.  
 FT DISULFID 125 138 BY SIMILARITY.  
 FT DISULFID 128 146 BY SIMILARITY.  
 FT DISULFID 149 164 BY SIMILARITY.  
 FT DISULFID 167 180 BY SIMILARITY.  
 FT DISULFID 170 188 BY SIMILARITY.  
 FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).  
 SO SEQUENCE 427 AA; 45183 MW; 809FA143FB3D625B CRC64;  
 Query Match 9.1%; Score 236; DB 1; Length 427;  
 Best Local Similarity 22.9%; Pred. No. 2.8e-08;  
 Matches 111; Conservative 62; Mismatches 194; Indels 118; Gaps 22;  
 QY 7 PGLILPLVLPALLADYVPGVQGLVPHPGDLERESPQGXNHPONSTICCTKCHKGT 66  
 DB 13 PRLILLLLGVSLGAKEA-----CPGLVYTH--SGECKACNLIGE 51  
 QY 67 YLVNDGCGPRDIDCRVCAAG-TYTALENLRRCSCSRCDMPQVEISPCVVDITYC 125  
 DB 52 GVADPC--GANOTVCEPCLDSVTFSDVSAITEPKCTECVG--IQSMGAPVEADDAVC 107  
 QY 126 GCRKNQYREYGEYGFRCINCSLCPNGT-VNIPQERODTIC-HCHMGFFLKAK-----C 179  
 DB 108 RC---AVGYQDETTRGRCACRYCEAGSGLVFCQDKONTVECCPDGYSDAANVDC 164  
 QY 180 ISCHDK-----NKECEKLCPT-----PSTGSDQDPGTVLLPLVIVRG 220  
 DB 165 LPCTVCEDETEROLRECTRWADACEBI-PGRWITRSTPEGSGSTAPSTOE--PEAPPEQ 221  
 QY 221 LCLASPVVLAACRYQWRPKYSLIICQSTLVKESEPELVAPGFNPTTTCFSTGS 280  
 DB 222 DLASTVAGVVT-----TWGSSOPVTRKTNNLPLV-----YCSIIA 260  
 QY 281 SSFVSIPIYI-----SCDRNFGVAASPSSETAPP-----HLKAGPILCPGPASTHLC 329  
 DB 261 AAVVGLVAVIAPKRWMSCKQKQGANRPVNTQPPREGKLSDSG--ISVDSGLHDOO 318  
 QY 330 PGPPASTHLCPPGPASTHLCPTPVQKWEASAPSDQDLADADPATLYAVVDGVPSPRWKE 389  
 DB 319 PHTQTASGQALKKGDLGVLSPPAKREVE-----KLINGSAGDPTMR 361  
 QY 390 LVRLGLIS-EHEIERLENGHRLREAOYSMLAAMRRTPREARETELGLRLQMDLLG 448  
 DB 362 LAGELGYQPEH-----IDSFTHCACPVRLALSW--ATQSATLLDALLAALRRIORD 412  
 QY 449 CLENI 453  
 DB 413 LVESL 417  
 RESULT 11  
 ID TR16\_RAT STANDARD; PRT; 425 AA.  
 AC P071174;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-  
 DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)  
 GN (p75 ICD) (Low affinity neurotrophin receptor p75NTR).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87115859; PubMed=3027580;  
 RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;  
 RT "Gene transfer and molecular cloning of the rat nerve growth factor  
 receptor.";  
 RL Nature 325:593-597 (1987).  
 RN (2)  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUEALIVER;  
 RA MEDLINE=93077038; PubMed=1446821;  
 RX "Regulatory elements and transcriptional regulation by testosterone  
 and retinoic acid of the rat nerve growth factor receptor promoter.";  
 RL Gene 121:247-254 (1992).  
 RN [3]  
 RP STRUCTURE BY NMR OF 334-418.  
 RX MEDLINE=97449145; PubMed=9305641; Ibanez C.F.;  
 RA Liepinsh E., Ilag L.V., Oetting G., Ibanez C.F.;  
 RT "NMR structure of the death domain of the p75 neurotrophin receptor.";  
 RL EMBO J. 16:4999-5005 (1997).  
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,  
 and NT-4. Can mediate cell survival as well as cell death of  
 neural cells.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-  
 associated cell death executor. Interacts with TRAF2, TRAF4 and  
 TRAF6 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: N- AND O-glycosylated.  
 CC -1- PTM: Phosphorylated on serine residues.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X05137; CAA28783.1.  
 DR EMBL: X61259; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: A26431; A26431.  
 DR PDB: INGR; 29-JUL-97.  
 DR InterPro: IPR000468; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death\_1.  
 DR Pfam: PF00020; TNFR\_c6; 4.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS00650; TNFR\_NGFR\_2; 4.  
 DR PROSITE: PS50017; DEATH DOMAIN; 1.  
 DR Receptor: Apoptosis; Neutrogenesis; Transmembrane; Glycoprotein;  
 KW Repeat; Phosphorylation; Signal; 3D-structure.  
 FT SIGNAL 1 29  
 FT CHAIN 1 425  
 FT FT 30 251  
 FT DOMAIN 252 273  
 FT TRANSMEM 274 425  
 FT DOMAIN 426 425  
 FT REPEAT 32 65  
 FT REPEAT 67 108  
 FT REPEAT 109 147  
 FT REPEAT 149 189  
 FT DOMAIN 190 419  
 FT DOMAIN 420 425  
 FT DISULFID 33 44  
 FT DISULFID 45 58  
 FT DISULFID 65 84  
 FT DISULFID 85 84

FT DISULFID 87 100 BY SIMILARITY.  
 FT DISULFID 90 108 BY SIMILARITY.  
 FT DISULFID 110 123 BY SIMILARITY.  
 FT DISULFID 126 139 BY SIMILARITY.  
 FT DISULFID 129 147 BY SIMILARITY.  
 FT DISULFID 150 165 BY SIMILARITY.  
 FT DISULFID 168 181 BY SIMILARITY.  
 FT DISULFID 171 189 BY SIMILARITY.  
 FT CARBOHYD 61 61 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 71 71 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 425 AA; 45432 MW; B2E152094D3827F8 CRC64;  
 Query Match 8.7%; Score 227.5; DB 1; Length 425;  
 Best Local Similarity 23.4%; Pred. No. 9, 8e-08;  
 Matches 107; Conservative 59; Mismatches 169; Indels 123; Gaps 24;  
 44 CPOGKYNHPQNSITICTCKHKGYLYNDCGPERDIDCRVCAFG-TYTALENHLRCLSC 102  
 33 CSTGLYTH---SGBCACVNLGEGVAQPC--GANQVCEPCLDNVTFSDVASATEPCPC 87  
 103 SRCDENFQVEISPCVDRDTVCGCRNQYREYMGTFGRCLNCSLCPNGT-VNIPQGR 161  
 88 TECUG--LQSMASAPCVADDAVCRGAVGYQD--EETG-HCEACSVCEVSGLVFSCQDK 142  
 162 QDTIC-HCHMGPFKAKGAK---CISCHCKKCEKCLPTPSTGKXSDP-PGTVLLPL 215  
 143 QNTVCEECPEGTYSDEANHYDPCLPCTVCEDE-RLQRECTPMADACEEIPG----- 194  
 216 VIVFGCLIASFASVAVLACRYQWKPKLYSIICGOSTLVKEGEPL---LYPAPGNTPT 270  
 195 -----RWIPRSTPEGSDTAPSTQBEVPEODLVSTVADMV 233  
 271 TTICFSSTP-----SSSPVSIPIYI-----SCDRSNFGVAVSPSE 306  
 234 TTWVGSSQPVVTRGTNDLIPVCSIIAAVVGAVIARKNRNSCKQKAGNSRPVNO 293  
 307 TAPP-----HLKAGPIIPGPASTHLCTPGPASTHLCTPGPA-----STHLCTPVQXW 356  
 294 TPPEGKRLKSDSG--ISVDSGLH-----DQTHQTNSGQLKQDGNLYSLPLTKR 345  
 357 EASAPAPDQADADPATLVAVVDGVPSPKKEIVRLGIS-EHEIRLSENRHLREA 415  
 346 E-----EVEKLLND-----TWRIHAGELGYQPEH-----IDSFTHACP 380  
 416 QYSMLAARRRTPRREATLELGRVLRDMDLGLCTENI 453  
 381 VRALLASWQAD---SATLDLALLAKRIQRADIVESL 415  
 RESULT 12  
 TR16\_MOUSE STANDARD: PRT: 417 AA.  
 ID TR16\_MOUSE  
 AC Q920W1.  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-  
 DE affinity nerve growth factor receptor) (NGF receptor) (low affinity  
 DE neurotrophin receptor p75NTR).  
 GN NGFR OR TNFRSF16.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_Taxid=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A;  
 RX MEDLINE=99077793; PubMed=9857182;  
 RA Tuffreau C., Benjean J., Blondel D., Kieffer B., Flaman A.;  
 RT "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a  
 RT receptor for rabies virus.";  
 RL EMBO J. 17:7250-7259 (1998).  
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,

CC AND NT-4. Can mediate cell survival as well as cell death of  
 CC neural cells (By similarity). Binds to rabies virus glycoprotein  
 CC Gs.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-  
 CC associated cell death executor. Interacts with TRAF2, TRAF4 and  
 CC TRAF6 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -1- PTM: N- AND O-glycosylated (By similarity).  
 CC -1- PTM: Phosphorylated on serine residues (By similarity).  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
 CC -----  
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 CC -----  
 CC EMBL: AF105292; AAD17943.1; -.  
 CC HSSP: P07174; INGR.  
 CC DR MGD; MGI:97323; Ngfr.  
 CC DR GO; GO:0005035; F:death receptor activity; IDA.  
 CC DR GO; GO:0005515; F:protein binding activity; IPI.  
 CC DR GO; GO:0007411; P:axon guidance; IMP.  
 CC DR GO; GO:0007417; P:central nervous system development; IMP.  
 CC DR GO; GO:0006917; P:induction of apoptosis; IDA.  
 CC DR InterPro; IPR004488; Death.  
 CC DR InterPro; IPR013368; TNFR\_C6.  
 CC DR Pfam; PF00531; death; 1.  
 CC DR Pfam; PF00020; TNFR\_C6; 4.  
 CC DR SMART; SM00208; TNFR; 1.  
 CC DR SMART; SM00208; TNFR; 3.  
 CC DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 CC DR PROSITE; PS00650; TNFR\_NGFR\_2; 4.  
 CC DR PROSITE; PS0017; DEATH DOMAIN; 1.  
 CC KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;  
 CC Repeat; Signal.  
 CC FT SIGNAL 1 21 BY SIMILARITY.  
 CC FT CHAIN 22 417 TUMOR NECROSIS FACTOR RECEPTOR  
 CC FT DOMAIN 22 246 SUPERFAMILY MEMBER 16.  
 CC FT TRANSMM 247 265 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 266 417 POTENTIAL.  
 CC FT REPEAT 24 57 CYTOPLASMIC (POTENTIAL).  
 CC FT REPEAT 57 100 TNFR-CYS 1.  
 CC FT REPEAT 101 100 TNFR-CYS 2.  
 CC FT REPEAT 101 139 TNFR-CYS 3.  
 CC FT REPEAT 141 181 TNFR-CYS 4.  
 CC FT REPEAT 141 181 DEATH.  
 CC FT DOMAIN 346 411 SER/THR-RICH.  
 CC FT DOMAIN 190 241 BY SIMILARITY.  
 CC FT DISULFID 25 36 BY SIMILARITY.  
 CC FT DISULFID 37 50 BY SIMILARITY.  
 CC FT DISULFID 40 57 BY SIMILARITY.  
 CC FT DISULFID 60 76 BY SIMILARITY.  
 CC FT DISULFID 79 92 BY SIMILARITY.  
 CC FT DISULFID 82 100 BY SIMILARITY.  
 CC FT DISULFID 102 115 BY SIMILARITY.  
 CC FT DISULFID 118 131 BY SIMILARITY.  
 CC FT DISULFID 131 139 BY SIMILARITY.  
 CC FT DISULFID 142 157 BY SIMILARITY.  
 CC FT DISULFID 160 173 BY SIMILARITY.  
 CC FT DISULFID 163 181 BY SIMILARITY.  
 CC FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).  
 CC SEQUENCE 417 AA; 44686 MW; 5074510DBAF982 CRC64;  
 CC -----  
 CC Query Match 8.5%; Score 221.5; DB 1; Length 417;  
 CC Best Local Similarity 23.1%; Pred. No. 2,3e-07;  
 CC Matches 106; Conservative 63; Mismatches 166; Indels 123; Gaps 26;  
 CC 44 CPOKHHHNSSTICCKKHKGYLVNDGPGGRTDRCVCAFG-TYTALENHARRCLSC 102  
 CC 25 CSTGMYTH---SGECACACNIGEGVAPC--GANOTVCEPCLDLSVFSDVSVATECKPC 79

QY 103 SRCRDENQVQISPCYVDRDVCGRKQRYREWGEFGRLNCSLCPNGT-VNIPQER 161  
 DB 80 TEGG--LQSNASACVEADAVCRCSGYVOD--EEFG-RCEACSVGSGSLVFSQDK 134  
 QY 162 QDTIC-HCHMGFPFKGAK---CISCHCK-----NKEKELCPFR----- 197  
 DB 135 QNTVCCECBETYSDEANHDPLCTVCEDETERQLRECTPMADAECEI-PCGWITRST 193  
 QY 198 PSTGKD-----SQDGTTLPLPLVIVFGLCLASFASVVLACRYQWRPKYISIIQOSTL 252  
 DB 194 PPEGSDVTPTSTQREAPPRDLI-----ASTV-----ADVTYTWGSSQPV 235  
 QY 253 VKGEPEPLVPAPFNFNTTICRSTSSSPVSIPIY-----SCDRNFGAVASPSSE 306  
 DB 236 VTRGTANLILPV-----YCSIIAAVGVIAVIAFKRMNSCKRQKQANSRPVQ 285  
 QY 307 TAPP-----HLKAGPLPGPASTHLCPTGPAPPA-----STHLCTPVQKW 356  
 DB 286 TPPEGEKHSDSG--ISVDSGLH-----DQHTHTQSAQALKGDKNLVSLPLTKR 337  
 QY 357 EASAPAPDQADADPATIYAVVGVPPSRKELVERLAGS-EHETERULENGRHLEA 415  
 DB 338 E-----EVEKLLNGD-----TWRIHAGELGYPEN-----IDSFTEACP 372  
 QY 416 QYSMLAAMRRRTPRREATTLELGRVLRDMDLGLCENI 453  
 DB 373 VRALLMSWGAQD--SATLDALLAALRRIQRADIVESTL 407  
 RESULT 13  
 ID TR16 CHICK STANDARD; PRT; 416 AA.  
 AC P18519;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-  
 DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)  
 DE (975 ICD) (low affinity neurotrophin receptor p75NTR).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=90166579; PubMed=2560385;  
 RA Large T.H., Weiskamp G., Heider J.C., Radeke M.J., Misko T.P.,  
 RA Shooter E.M., Reichardt L.F.;  
 RT "Structure and developmental expression of the nerve growth factor  
 RT receptor in the chicken central nervous system."; Neuron 2:1123-1134(1989).  
 RN [2]  
 RP SEQUENCE OF 21-416 FROM N.A.  
 RX MEDLINE=90152140; PubMed=2154393;  
 RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;  
 RT "Structure and developmental expression of the chicken NGF receptor.";  
 RT Dev. Biol. 137:287-304(1990).  
 CC -1- FUNCTION: low affinity receptor which can bind to NGF, BDNF, NT-3,  
 CC and NT-4. Can mediate cell survival as well as cell death of  
 CC neural cells (By similarity).  
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-  
 CC associated cell death executor. Interacts with TRAF2, TRAF4 and  
 CC TRAF6 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: N- AND O-glycosylated.  
 CC -1- PTM: Phosphorylated on serine residues.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
 CC PIR; JN0006; JN0006.

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DR HSPB, P07174; INGR.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF000531; death_1.
DR Pfam; PF000202; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00650; TNFR_NGFR_2; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW Repeat; Phosphorylation; Signal.
FT CHAIN 1 19
FT SIGNAL 20 416
FT DOMAIN 29 239
FT TRANSMEM 240 261
FT DOMAIN 262 416
FT REPEAT 23 57
FT REPEAT 58 99
FT REPEAT 100 138
FT REPEAT 140 180
FT DOMAIN 188 410
FT DOMAIN 188 236
FT DISULFID 36 49
FT DISULFID 39 56
FT DISULFID 59 75
FT DISULFID 78 91
FT DISULFID 81 99
FT DISULFID 101 114
FT DISULFID 117 130
FT DISULFID 120 138
FT DISULFID 141 156
FT DISULFID 159 172
FT DISULFID 162 180
FT CARBOHYD 52 52
FT CONFLICT 36 36
FT CONFLICT 173 173
FT CONFLICT 276 276
FT CONFLICT 396 396
SQ SEQUENCE 416 AA; 44654 MW; 6BCEAB54F4AD2D56 CRC64;

Query Match 8.5%; Score 220; DB 1; Length 416;
Best Local Similarity 23.3%; Pred. No. 2,9e-07;
Matches 116; Conservative 46; Mismatches 168; Indels 168; Gaps 25;

6 VPGLLPLVLPALLADVYAGVGLVPHGDLKRESPPCKGKYNHPNSTICCTKCHKG 65
5 VPLLLLL-----PAG-----PTWGSKEK-----CLTKMYT---TSGCCCKACNIG 42
66 TVLVNDCPGRGRTDCRCVAPG-TYALLENHLRLRCSCSRCDMDQVSLPCVYNDRTV 124
43 EGVAVPC--GVNQTVCERCLDSVTYSDYVATPRCTQCVG--LHSMAPCVESDDAV 98
125 CGRKNQYREYMGEGFRCLNGSLCPNG-TVINPCOBROPTIC-HCHMGFFLKAGK---- 178
99 CRC---AYGTFDELSSCKECSICEVGRGLMFPCCDSQDTVEBCEGFSDEANFVVP 155
179 CISCCHCK-----NKECEKLCF-----TRPSTGKDSQDPGT-----T 210
156 CLPCTCICEBENWVWKECTATSDAECRDILHPRMTTHPISLAGSDSPFITDPEFTEGMAT 215
211 VLLPLVVFGLCLASFASVVLACRYQWRKLYSIICGOSTLYKEBPELIVAPGFNPT 270
216 TLADIIV-----TWGSSQPVVSRKADLVLLIV----- 243
271 TTICFSSTPSSPVSIPIYI-----SCDRSNFGAVALSPSESTAPP-----HLKAGPIIP 319
244 ----YCSITLAUVGVGLVAVIAPKRMNSCKKNGKCANRPVNGPSPBEGKLIHSDGISVD 299
320 GPAPASTHCTPGPAPASTHCTPGPAPASTHCTPVQKWEASAFAPQDLADADPATIYAVV 379

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Db 300 ----SQSLHDOQPPNOS---TQGP-----APKDGSLVA-- 326
OY 380 DGVPPSR-----WKELVRLGLSEHEIERLEJENGRHLNEAGYSMLAAR 424
Db 327 -SLPSPKQEVERKVLSSSAEETWRQLAGELGYKEDLIDCFTR-----ESPALADN- 379
OY 425 RRTPRREATLELIGRVLR 442
Db 380 --SAKETATIDLALVLR 395

RESULT 14
TRIB HUMAN
ID TRIB HUMAN STANDARD; PRT; 461 AA.
AC P20333; Q16042; Q9U1H1;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept)
DE [Contains: Tumor necrosis factor binding protein 2 (TBPII)].
GN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=90260639; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins.";
RL Science 248:1019-1023(1990).
[2]
SEQUENCE FROM N.A. AND VARIANT ARG-196.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=96299745; PubMed=8661109;
RA Bellingier C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepanlier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
[4]
SEQUENCE OF 37-461 FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
RA Brockhaus M., Leeseleuer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytokine 2:231-237(1990).
[5]
SEQUENCE OF 116-461 FROM N.A. PARTIAL SEQUENCE, AND VARIANT ARG-196.
RX MEDLINE=90349572; PubMed=2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
[6]
SEQUENCE OF 154-183 FROM N.A. AND VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21069356; PubMed=11197692;
RA Tauchiya N., Komatsu T., Macsushita M., Ohashi J., Tokunaga K.;
RT "New single nucleotide polymorphisms in the coding region of human
RT TNFR2: association with systemic lupus erythematosus.";
RL Genes Immun. 1:501-503(2000).

```



QY 264 ARGNPPTTICSSSPSS-----PVSIPIYICSDNSNGAVASPSSETPAPHLKAGPILP 319  
 DB 190 IPGNASMAVCTISPTSRMAPGAVHLPQVSTRSQHTPTPEPS--TAPSTSFLLMGP 247  
 QY 320 GPPA 323  
 DB 248 GPPA 251

RESULT 15  
 TR23\_MOUSE STANDARD; PRT; 176 AA.  
 AC Q9ER63; OSVHC0;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB).  
 GN TNFRSF23 OR TNFRSF1A1 OR TNFRH1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV; TISSUE=Embryonic stem cells;  
 RX MEDLINE=20519229; PubMed=11063728;  
 RA Engemann S., Stredlicke M., Paulsen W., Franck O., Reinhardt R., Lane N., Reik W., Walter J.;  
 RT "Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting."; Hum. Mol. Genet. 9:2691-2706(2000).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RA Pan G., Mao W., Ribser P.;  
 RT "Characterization of SOB, a member of the TNFR family."; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RL -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: Ubiquitous.  
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AJ278264; CAC16405.1; -;  
 DR EMBL; AJ278505; CAC27352.1; -;  
 DR EMBL; AY046550; AAL05072.1; -;  
 DR HSSP; P19438; 1EXT.  
 DR MGD; MGI:1930269; Tnfra23.  
 DR InterPro; IPR001368; Tnfra23.  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.  
 FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 10 30 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).  
 FT DOMAIN 31 176 EXTRACELLULAR (POTENTIAL).  
 FT REPEAT 37 72 TNFR-CYS 1.  
 FT REPEAT 74 114 TNFR-CYS 2.  
 FT REPEAT 115 155 TNFR-CYS 3.  
 FT DIDULFD 38 49 BY SIMILARITY.  
 FT DISULFD 50 63 BY SIMILARITY.  
 FT DISULFD 53 72 BY SIMILARITY.  
 FT DISULFD 75 90 BY SIMILARITY.  
 FT DISULFD 93 106 BY SIMILARITY.

FT DISULFD 96 114 BY SIMILARITY.  
 FT DISULFD 116 131 BY SIMILARITY.  
 FT DISULFD 134 147 BY SIMILARITY.  
 FT DISULFD 137 155 BY SIMILARITY.  
 FT CARBOHYD 148 148 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 176 AA; 19594 MW; EE30D617F49DD87D CRC64;

Query March 7.5%; Score 196; DB 1; Length 176;  
 Best Local Similarity 31.1%; Pred. NO. 4e-06;  
 Matches 51; Conservative 18; Mismatches 63; Indels 32; Gaps 8;

QY 9 LLLPLVLPALADYVPAVGQGLVPHPGDLEKRESPCPGKYNHPNNTICTCKHGTYL 68  
 DB 18 LLLPLVLPVIFA-----MP-----ESYFNCPDGEY---QSNVCCCKTCPSGTFV 59  
 QY 69 YNDCEPGRDTCVCAFGTYTALENHRLSCSRCDENFQVEISFCVVDRTVCGCR 128  
 DB 60 KAPCKIPHTQGCCKCHGFTGKDNGLHDELCTCDKD--QNMVADCSATSDRKCEC- 116  
 QY 129 KQYREYWGEGTF--RCINCSLCFNGTYNIP-----CQERODTIC 166  
 DB 117 --QIGLYYDPEKFPESCPCTKCPG--IPVLOECNSTANTVVC 155

Search completed: September 13, 2003, 07:04:40  
 Job time : 18 secs



• Tue Sep 16 09:11:47 2003

US-09-970-532-2.rpt

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2003, 07:01:54 ; Search time 39 Seconds

(without alignments)  
3116.481 Million cell updates/sec

Title: US-09-970-532-2

Perfect score: 2603  
Sequence: 1 MGLPTVPGLLPLVLPAALLA.....NIEBALGASARIASEPRLLW 471

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_archaea:\*  
2: SP\_bacteria:\*  
3: SP\_fungi:\*  
4: SP\_human:\*  
5: SP\_invertebrate:\*  
6: SP\_mammal:\*  
7: SP\_mhc:\*  
8: SP\_organelle:\*  
9: SP\_plant:\*  
10: SP\_rodent:\*  
11: SP\_virus:\*  
12: SP\_vertebrate:\*  
13: SP\_unclassified:\*  
14: SP\_virus:\*  
15: SP\_bacteriophage:\*  
16: SP\_bacteriophage:\*  
17: SP\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1589.5	61.1	446	6	Q95ND3
2	790	30.3	189	6	Q95185
3	776	29.8	189	6	Q97530
4	400.5	15.4	413	11	Q99MM1
5	360	13.8	387	11	Q99MM1
6	220.5	8.5	417	11	Q8VD70
7	220.5	8.5	427	11	Q8BY11
8	211.5	8.1	368	13	Q57408
9	210	8.1	368	13	Q57408
10	206.5	7.9	387	13	Q91AR7
11	201.5	7.7	433	11	Q91ZM6
12	200	7.7	368	13	Q9PW79
13	199.5	7.7	651	13	Q98SM6
14	191	7.3	322	12	Q72761
15	187.5	7.2	302	13	Q9PUS0
16	187.5	7.2	357	13	Q9DF34

17	185.5	7.1	283	6	Q9XZ8	Q9XZ8 cercopithec
18	185	7.1	320	12	Q57079	Q57079 compox viru
19	180.5	6.9	401	13	Q9PRG7	Q9PRG7 xenopus lae
20	178	6.8	350	12	Q57123	Q57123 compox viru
21	177.5	6.8	267	6	Q02764	Q02764 oryctolagus
22	176	6.8	347	12	Q57119	Q57119 compox viru
23	176	6.8	351	12	Q57121	Q57121 compox viru
24	175	6.7	360	12	Q57118	Q57118 compox viru
25	174	6.7	316	12	Q57092	Q57092 ectromelia
26	174	6.7	317	13	Q8JFV6	Q8JFV6 brachydanio
27	174	6.7	320	12	Q57091	Q57091 ectromelia
28	174	6.7	320	12	Q57300	Q57300 ectromelia
29	173.5	6.7	289	11	Q8K2X6	Q8K2X6 mus musculu
30	173.5	6.7	347	12	Q57115	Q57115 compox viru
31	173	6.6	459	11	Q62327	Q62327 mus musculu
32	172	6.6	351	12	Q57117	Q57117 compox viru
33	172	6.6	438	13	Q9DFV0	Q9DFV0 brachydanio
34	169.5	6.5	349	12	Q57305	Q57305 compox viru
35	169	6.5	326	12	Q57122	Q57122 compox viru
36	168.5	6.5	482	11	Q88734	Q88734 mus musculu
37	165	6.3	457	4	Q81V86	Q81V86 homo sapien
38	164.5	6.3	349	12	Q57109	Q57109 variola vir
39	164	6.3	547	5	Q818V2	Q818V2 giardia lam
40	164	6.3	547	5	Q818V1	Q818V1 giardia lam
41	163.5	6.3	320	6	Q9X829	Q9X829 oryctolagus
42	163.5	6.3	348	12	Q57112	Q57112 variola vir
43	163.5	6.3	349	12	Q57111	Q57111 variola vir
44	163.5	6.3	349	12	Q57098	Q57098 camelpox vi
45	163.5	6.3	349	12	Q57284	Q57284 camelpox vi

#### ALIGNMENTS

RESULT 1  
Q95ND3 PRELIMINARY; PRT; 446 AA.  
ID Q95ND3  
AC Q95ND3;  
DT 01-DEC-2001 (TRENBLER, 19, Created)  
DT 01-DEC-2001 (TRENBLER, 19, Last sequence update)  
DT 01-MAR-2003 (TRENBLER, 23, Last annotation update)  
DE Tumor necrosis factor type I.  
GN TNFR I.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RX [1]  
RP SEQUENCE FROM N.A.  
RA Mizuno T., Goto Y., Baba K., Maeda K., Ohno K., Tsunimoto H.;  
RT "Molecular cloning of feline tumor necrosis factor receptor type I  
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in  
RT cats.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB051103; BAB55455.1;  
DR InterPro; IPR000345; CytC\_heme\_bind.  
DR InterPro; IPR006209; Death.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00190; CYTOCHROME C; 1.  
DR PROSITE; PS00017; DEATH DOMAIN; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS00650; TNFR\_NGFR\_2; 3.  
SQ SEQUENCE 446 AA; 49563 MW; 217BD331DDBA74AA CRC64;

Query Match 61.1%; Score 1589.5; DB 6; Length 446;  
Best Local Similarity 66.0%; Pred. No. 1e-125;  
Matches 311; Conservative 39; Mismatches 94; Indels 27; Gaps 6;

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QY 1 MGLPTVPGLLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGQKYNHPONSTICT 60
DB 1 MGLPTVPGLLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGQKYNHPONSTICT 60
QY 61 KCHKGTLYLNDPCPGRDTDCRVCAPGTYTALLENHRLRCLSCSRCDMEFVVEISPCVVD 120
DB 61 KCHKGTLYLNDPCPGRDTDCRVCAPGTYTALLENHRLRCLSCSRCDMEFVVEISPCVVD 120
QY 121 RDVTCGCRKNQRYRYWSEBTHFCQCLNCSLCLNGTVQISCKEONTVCTCHAGFFLRGNECV 180
DB 121 RDVTCGCRKNQRYRYWSEBTHFCQCLNCSLCLNGTVQISCKEONTVCTCHAGFFLRGNECV 180
QY 181 SCHDC-KKKECEKLCPTPSTGKSDODPGTTLVLPVLPVFGILCLASPAVVLACRYORWK 239
DB 181 SCHDC-KKKECEKLCPTPSTGKSDODPGTTLVLPVLPVFGILCLASPAVVLACRYORWK 239
QY 240 PKLVSIICGOSTLVGEGBELVLPAPGFNPTTTCFSSSTPSSPVSIPIYISCDRSMFGA 299
DB 240 PKLVSIICGOSTLVGEGBELVLPAPGFNPTTTCFSSSTPSSPVSIPIYISCDRSMFGA 299
QY 298 -ASVSRMAPPYOGAGPILSA PASG-----PIS-----TPVQKWDSDS 334
DB 298 -ASVSRMAPPYOGAGPILSA PASG-----PIS-----TPVQKWDSDS 334
QY 360 APSADQDLADDPATLVAVVGVPPSRMKEIVRLGLSEHEIERLEENGRHLREAOYSM 419
DB 360 APSADQDLADDPATLVAVVGVPPSRMKEIVRLGLSEHEIERLEENGRHLREAOYSM 419
QY 420 LAAMRRRTPRREATLELLGRVLRDMDLGCLNIEBALGGAARLASERPLL 470
DB 420 LAAMRRRTPRREATLELLGRVLRDMDLGCLNIEBALGGAARLASERPLL 470
QY 470 LAAMRRRTPRREATLELLGRVLRDMDLGCLNIEBALGGAARLASERPLL 470
DB 470 LAAMRRRTPRREATLELLGRVLRDMDLGCLNIEBALGGAARLASERPLL 470
```

```
RESULT 2
Q95185 PRELIMINARY; PRT; 189 AA.
AC 095185;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Tumor necrosis factor receptor p60 (fragment).
GN TNFR-1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OC NCBI_TaxId=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Duchie S., Nasir L., Eckersall P.D.;
RT "Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,
RT partial cds."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.
DR HSSP; P19438; 1TNR.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KM Receptor.
FT NON_TER
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;
```

```
Query Match 30.3%; Score 790; DB 6; Length 189;
Best Local Similarity 73.1%; Pred. No. 9, 2e-59;
Matches 136; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
```

```
QY 61 KCHKGTLYLNDPCPGRDTDCRVCAPGTYTALLENHRLRCLSCSRCDMEFVVEISPCVVD 120
DB 61 KCHKGTLYLNDPCPGRDTDCRVCAPGTYTALLENHRLRCLSCSRCDMEFVVEISPCVVD 120
QY 121 RDVTCGCRKNQRYRYWSEBTHFCQCLNCSLCLNGTVQISCKEONTVCTCHAGFFLRGNECV 180
DB 121 RDVTCGCRKNQRYRYWSEBTHFCQCLNCSLCLNGTVQISCKEONTVCTCHAGFFLRGNECV 180
QY 181 SCHDC 186
DB 181 SCHDC 186
```

```
RESULT 3
Q97530 PRELIMINARY; PRT; 189 AA.
AC 097530;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Tumor necrosis factor receptor p60 (fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Brain;
RX MEDLINE=21109092; Pubmed=1102158;
RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duchie S.,
RA Bennett D.;
RT "Cloning of canine IL-1ra, TNFR and TIMP-2."
RL Vet. Immunol. Immunopathol. 78:207-214(2001).
DR EMBL; AF013955; AAD01516.1; -.
DR HSSP; P19438; 1TNR.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KM Receptor.
FT NON_TER
SQ SEQUENCE 189 AA; 21324 MW; 5D3AD6A5676BFE99 CRC64;
```

```
Query Match 29.8%; Score 776; DB 6; Length 189;
Best Local Similarity 73.1%; Pred. No. 1, 4e-57;
Matches 136; Conservative 15; Mismatches 35; Indels 0; Gaps 0;
```

```
QY 1 MGLPTVPGLLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGQKYNHPONSTICT 60
DB 1 MGLPTVPGLLLPLVLPALLADVPAGVGLVPHPGDLEKRESPPCGQKYNHPONSTICT 60
QY 61 KCHKGTLYLNDPCPGRDTDCRVCAPGTYTALLENHRLRCLSCSRCDMEFVVEISPCVVD 120
DB 61 KCHKGTLYLNDPCPGRDTDCRVCAPGTYTALLENHRLRCLSCSRCDMEFVVEISPCVVD 120
QY 121 RDVTCGCRKNQRYRYWSEBTHFCQCLNCSLCLNGTVQISCKEONTVCTCHAGFFLRGNECV 180
DB 121 RDVTCGCRKNQRYRYWSEBTHFCQCLNCSLCLNGTVQISCKEONTVCTCHAGFFLRGNECV 180
QY 181 SCHDC 186
DB 181 SCHDC 186
```

```
RESULT 4
Q99MM1 PRELIMINARY; PRT; 413 AA.
AC 099MM1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
```

DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)  
 DE WSL-1-like protein.  
 GN TNFRSF25 OR TNFRSF12.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv;  
 RK MEDLINE=21158384; PubMed=11261933;  
 RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farow S.N.,  
 RA Owen M.J.;  
 RT "Genomic structure, expression, and chromosome mapping of the mouse  
 RT homologue for the WSL-1 (DR3, Ap03, TRAMP, LARD, TR3, TNFRSF12)  
 RT gene";  
 RL Immunogenetics 53:59-63(2001).  
 DR EMBL; AF329969; AK11256.1; -.  
 DR HSSP; Q92956; JUMA.  
 DR MGD; MGI:193467; Tnftrf25.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SMO0005; DEATH; 1.  
 DR SMART; SMO0208; TNFR; 3.  
 DR PROSITE; PS50017; DEATH DOMAIN; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
 SQ SEQUENCE 413 AA; 44453 MW; 69F21B85DDADABAF CRC64;  
 Query Match 15.4%; Score 400.5; DB 11; Length 413;  
 Best Local Similarity 27.9%; Pred. No. 1,5e-25;  
 Matches 135; Conservative 47; Mismatches 175; Indels 127; Gaps 21.  
 QY 9 LLLPLVLLALLADVYPAGVGVLPHPGDLERKESPCPGQKYNHNPSTICTCKCHKGYL 68  
 DB 18 LLLLLLLLLLGGQGGGMSGRGDCASSQKRYG-----FCRCGCKGHY 64  
 QY 69 YNDGCGRGDIDCRKACPGTYALENNLRR-CLSCSRGDEMFOVEISPCVVDRTVCGC 127  
 DB 65 KAPCAEPGNSSTCLPSPSDTFLTRDNNFKTDCTRCQVCDDEALQVTLNCSAKSDTHGCG 124  
 QY 128 RKNQRYREYVGEGTGFRLCNSLCPNGTV---IPC-----QEQGLICHMGFPLKGA 178  
 DB 125 QSG-----W-----CVDCTVPGCKSPSCPSFCVPGCATTPVHEAFTPRPLCPGFIKND 173  
 QY 179 CISCCHDCNKKCEKLCPTRPSTGKDSQDPGTVLLPLVIVFGLCLASFAVYLACRYQWR 238  
 DB 174 CTSCPRTGSSVCPKAC-TAVCGWK--QMFVQVILGVAFRG-----AIIICAYRW 222  
 QY 239 KPKLYSIICGGSTLVKEGPELIVAPAFNPPTTTCISFSTSSSPVSIPIITICDRSNFG 298  
 DB 223 Q-----PCKAVTVADTGTETELASP----- 242  
 QY 299 AVASPSSETAPPHLKAGP--ILDGPAST-HLC-----TPGPASTH-LC----- 339  
 DB 243 -----QTA--HLSASDSATLLAPPESTGKICTTVQVLGNMNTPLGSLQYQVCGAS 293  
 QY 340 -----TPGPASTHLCCTVQCKEASAPAPQLADADA-PLIYAVDGVPPSRMKELYR 393  
 DB 294 QPMQLPRTITGTPASPL---SPAPAGSPAIVLQGPOLYVMAVAPARMKETFEFT 349  
 QY 394 LGLSEHEIIRLELENGRLREAOYSMLAAMRRTPRREATLELGRVLRDDDLGGLCENI 453  
 DB 350 LGLREAEIRIYAVEVEICR-FRDQYVEMLRWQQGP--AGLGAITYALERGLSGCAEDL 405  
 QY 454 EEL 457  
 DB 406 RSRLL 409

ID	PRELIMINARY	PRT	387 AA
08VD70			
01-MAR-2002	(TREMBLER). 20, Created)		
01-MAR-2002	(TREMBLER). 20, Last sequence update)		
01-MAR-2003	(TREMBLER). 23, Last annotation update)		
Similar to tumor necrosis factor receptor superfamily, member 12.			
TFNRSF5 OR TFNRSF12.			
Mus musculus (Mouse).			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10090;			
NCBI_TaxID=10090;			
SEQUENCE FROM N. A.			
TISSUE=Salivary gland;			
Strasbourg R.			
Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.			
EMBL; BC017526; AAI17526.1; -			
MGD; MGI:193467; Tinftr25.			
InterPro; IPR000488; Death.			
InterPro; IPR006209; EGF_1ike.			
InterPro; IPR01368; TNFR_C6.			
Plan; PF00531; Death; 1.			
Plan; PF00020; TNFR_C6; 2.			
SMART; SM00005; DEATH; 1.			
SMART; SM00208; TNFR; 2.			
PROSITE; PS50017; DEATH DOMAIN; 1.			
PROSITE; PS01186; EGF_2; 1.			
PROSITE; PS00652; TNFR_NGFR_1; 1.			
PROSITE; PS50050; TNFR_NGFR_2; 1.			
Receptor.			
SEQUENCE 387 AA; 41640 MW; P1664466BAD68D3 CRC64;			
Query Match	13.8%; Score 360; DB 11; Length 387;		
Best Local Similarity	27.0%; Pred. No. 3.7e-22;		
Matches 130; Conservative 46; Mismatches 161; Indels 144; Gaps 22;			
01	PG-----LPLPLVLLALLADVYPAGVGLVPHRPGLEKRESPPQGVKYNHNPQSTICCKK	62	
02	17 PGSTAVRLQPLFLPULLLLLLLLGGG-----QGMGSR-----CDCASSQKRYGPPCCRCG	69	
03	63 HKGYLLYNDGPGRDTDCRYCAGDTYALENHLR-CLSCRCRDEMFOYEISPCVYDR	121	
04	70 PKGYHMAKPCAEPCGNSCTLPCPSDFLTRDNHFKTCTRCQVCDDEALQVTLNCSAKS	129	
05	122 DTVGCGKKNQRYREWGTGTRCLNCSLCRPNQTV-----IPQGEQDITICHGMGFPFLKGA	177	
06	130 DTHGCGGSG-----W-----CVDGSTPECKSKSPSCVPC-----GA	161	
07	178 KCISCHDCKNKECKLCPTPESTCKSQDQDPTVLLPLVLVIFGLCLASFASVVLACRYOR	237	
08	162 -----TPVHEAPRLPLFMVQVLLGVAFLLG-----AIIICAYCR	195	
09	238 MKP---KLYSILICQSTL-----VKSGEPFLVPAPGFNPTT--ICFSS-----	277	
10	196 WQPKAVVAVDTAGETELTASPTQAHLSASDSAHTLAP-----PSSYGIKICTTVQLVGN	250	
11	278 -TSSSPVSIPIPYISCDRNSFGAVASPSSETPAPHLKAGPILPQPPASTHLCITGPPAST	336	
12	251 WTPELSGTQ--EYVCGQASQPMQDLNRLGLTP--LASPLSPAPRA-----GSPAA--	297	
13	337 HLCITGPPASTHLCITPVQKWEASAPAPDOLADPATLTYAVVDGVPSSKVELVRLGL	396	
14	298 -VLOPGP-----QLVDVDAVDAPARWKEPFVRLTGL	326	
15	397 SEHIELELENGRHLREAOYSMLAAMRRTPREATLIELGLVLRMDLGLCENIEEA	456	
16	327 REAEIEAVVEICR-FRDOOYEMIKKRRQOP--AGLGAIVALLERMGLEGCAEDLR	382	
17	457 L 457		

Db 383 L 383

## RESULT 6

ID Q8BY1 PRELIMINARY; PRT; 417 AA.

AC Q8BY1; 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Tumor necrosis factor receptor 16.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; Tissue=Skin;  
 RX MEDLINE=22354683; PubMed=12466651;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK037248; BAC29775.1; --  
 SO SEQUENCE 417 AA; 44672 MW; CD0440E7E70A617 CRC64;

Query Match 8.5%; Score 220.5; DB 11; Length 417;

Best Local Similarity 23.1%; Pred. No. 2,3e-10;

Matches 106; Conservative 63; Mismatches 166; Indels 123; Gaps 26;

QY 44 CPOGKYNHPONSTICTCKCHKGTLYVNDGPGRGDTDCRVCAPO-TYTALENHLRCLSC 102  
 DB 25 CSTGMVTH---SGECCACNLGEGVAQPC--GANQTVCEPCLDSVTFSDVVSATEPCPKC 79  
 QY 103 SGRCDMEFYEISFCVYDRDVTGCGKKNQYREYMGTEGFRCLNCLCPNGT-VNIPCOER 161  
 DB 80 TECLG--LQSMAPCEADDAVAVCRCSYGYOD--EETG-RCEACSVCGVSGLVFSCQDK 134  
 QY 162 ODTIC-HCHMGFFLKAK-----CISCHDK-----NKECEKLCPTR----- 197  
 DB 135 QNTVCEBCEBGTYSDEANHVDPCLPCTVCEDETEROLRECTPMADAECEI-PGRWITRST 193  
 QY 198 PSTGKD-----SQDPTVLLPLVIFGLCLASFAVLAORYKPKLYIICGOSTL 252  
 DB 194 PREGSDVTTPTGPEAPPERDLI-----ASTV-----ADVTVTVMGSSQPV 235  
 QY 253 VKEGPELLVAPGFNPTTTCFSSSTSSSPVSIPIYI-----SCDRNFGVAAPSSSE 306  
 DB 236 VTRGTADNLIPIV-----YCSILAAVVGVAIYAFKRWNSCKONKQANSRPVNO 285  
 QY 307 TAPP-----HLKAGPILPGPPASTHLCTGPPASTHLCTGPPA-----STHLCTPVOKW 356  
 DB 286 TPPEGEKLSHDSG--ISVDSQSLH-----DQDHTOTASGQALKDGNLYSLPLTKR 337  
 QY 357 EASAPADQADADPATLYAVVDGVPSPRWKELVRRIGLS-EHEIERLELNGRHLEA 415  
 DB 338 E-----EVEKLLNGD-----TWRIHLAGELGYOPRH-----IDSEFTHEACP 372  
 QY 416 QYSMLAAMRRRTPRREATLLELGRVLRDMDLGCLENI 453  
 DB 373 VRALLASWGAQD---SATLDLALALRRIORADIVESL 407

## RESULT 7

ID Q8CFT3 PRELIMINARY; PRT; 427 AA.

AC Q8CFT3; 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Similar to nerve growth factor receptor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC Tissue=Eye;

RA Strausberg R.;

RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC038365; AAH38365.1; --

KW Receptor.

SO SEQUENCE 427 AA; 45647 MW; 7AC73263F7B31436 CRC64;

Query Match 8.5%; Score 220.5; DB 11; Length 427;

Best Local Similarity 23.1%; Pred. No. 2.4e-10;

Matches 106; Conservative 63; Mismatches 166; Indels 123; Gaps 26;

QY 44 CPOGKYNHPONSTICTCKCHKGTLYVNDGPGRGDTDCRVCAPO-TYTALENHLRCLSC 102  
 DB 35 CSTGMVTH---SGECCACNLGEGVAQPC--GANQTVCEPCLDSVTFSDVVSATEPCPKC 89  
 QY 103 SGRCDMEFYEISFCVYDRDVTGCGKKNQYREYMGTEGFRCLNCLCPNGT-VNIPCOER 161  
 DB 90 TECLG--LQSMAPCEADDAVAVCRCSYGYOD--EETG-RCEACSVCGVSGLVFSCQDK 144  
 QY 162 ODTIC-HCHMGFFLKAK-----CISCHDK-----NKECEKLCPTR----- 197  
 DB 145 QNTVCEBCEBGTYSDEANHVDPCLPCTVCEDETEROLRECTPMADAECEI-PGRWITRST 203  
 QY 198 PSTGKD-----SQDPTVLLPLVIFGLCLASFAVLAORYKPKLYIICGOSTL 252  
 DB 204 PREGSDVTTPTGPEAPPERDLI-----ASTV-----ADVTVTVMGSSQPV 245  
 QY 253 VKEGPELLVAPGFNPTTTCFSSSTSSSPVSIPIYI-----SCDRNFGVAAPSSSE 306  
 DB 246 VTRGTADNLIPIV-----YCSILAAVVGVAIYAFKRWNSCKONKQANSRPVNO 295  
 QY 307 TAPP-----HLKAGPILPGPPASTHLCTGPPASTHLCTGPPA-----STHLCTPVOKW 356  
 DB 296 TPPEGEKLSHDSG--ISVDSQSLH-----DQDHTOTASGQALKDGNLYSLPLTKR 347  
 QY 357 EASAPADQADADPATLYAVVDGVPSPRWKELVRRIGLS-EHEIERLELNGRHLEA 415  
 DB 348 E-----EVEKLLNGD-----TWRIHLAGELGYOPRH-----IDSEFTHEACP 382  
 QY 416 QYSMLAAMRRRTPRREATLLELGRVLRDMDLGCLENI 453  
 DB 383 VRALLASWGAQD---SATLDLALALRRIORADIVESL 417

## RESULT 8

ID O57408 PRELIMINARY; PRT; 368 AA.

AC O57408; 01-JUN-1998 (Tremblrel. 06, Created)  
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Subgroup B AIV receptor.  
 OS Meleagris gallopavo (Common turkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=97471016; PubMed=9326659;  
 RX Adkins H.B., Brojatchek J., Naughton J., Rolfs M.M., Resola J.M.,  
 RA Young J.A.;  
 RT "Identification of a cellular receptor for subgroup B avian leukosis  
 virus".  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622(1997).  
 DR EMBL; AF006002; AAB93987.1; --  
 DR HSSP; O14763; 1D0G.  
 DR InterPro; IPR001450; 4Fe4s\_ferredoxin.







DR PÉam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00208; TNFR\_2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00650; TNFR\_NGFR\_2; 2.  
SQ SEQUENCE 322 AA; 35412 MW; 774549278D156A9D CRC64;

Query Match 7.3%; Score 191; DB 12; Length 322;

Best Local Similarity 31.4%; Pred. No. 5.3e-08;  
Matches 49; Conservative 18; Mismatches 71; Indels 18; Gaps 7;

QY 27 VGLVPHPDGDEKRSPPCGKYNPNSTICTCKHKTYLYNDPCGGRDTCRCVAP 86  
DB 18 VSGDVPY---EHNGKCKGTIDYNSNN-LCKKQCDPGMYTHSC-NTSNTKCAKCPD 71  
QY 87 GTTALLENHTRRLSC-SRCDREMPQVEISPCVVDRTVCGCRKNQREYWGEGTSPR-CL 144  
DB 72 GTFTSIPNHIPTCLSGRKCASN--QVETKSCSNTQDRECVACASGYCEFGSNGCRLLCV 129  
QY 145 NCSLCPNGTVNIPCOBRDPTIC-----HCHMGF 172  
DB 130 PQTCKDSGYGVYGSKGDVICKKCPGNIDKCMDSF 165

RESULT 15

Q9PUS0 PRELIMINARY; PRT; 302 AA.

AC Q9PUS0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Decoy TNF receptor.  
OS Salvelinus fontinalis (Brook trout) (Brook char).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.  
OX NCBI\_TaxId=8038;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20111091; PubMed=10642582;  
RA Bobe J., Goetz F.W.;  
RT "A tumor necrosis factor receptor homologue is up-regulated in  
RT the brook trout (Salvelinus fontinalis) ovary at the completion of  
RT ovulation.";  
RL Biol. Reprod. 62:420-426(2000).  
DR EMBL; AF156738; AAD56428.1; -.  
DR HSSP; Q14763; 1D4V.  
DR InterPro; IPR006209; EGF\_1like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR PÉam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00208; TNFR\_2; 4.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00650; TNFR\_NGFR\_2; 1.  
KW Receptor.  
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 7.2%; Score 187.5; DB 13; Length 302;

Best Local Similarity 28.7%; Pred. No. 9.7e-08;  
Matches 52; Conservative 18; Mismatches 60; Indels 51; Gaps 10;

QY 56 TICTCTCHKTYLYNDPCGGRDTCRCVAPGTYTALLENHTRRLSCSRCDREMPQVEIS 115  
DB 33 SIYCDRCPPTPTVIRAPPSAM-RKSDCAECNPAVTEFWNHSKCLRCSCWCAEN--QVYKQ 89  
QY 116 PCVVDRTVCGCRKNQY--REYWGEGTFRCLNCSLCPNG---TVNIPCOBRDPTIC-HC 168  
DB 90 ECSPSNKCECECKEGYFNKKYEA-----CIKHKECPGAGANTTGT---HQDTCEVQC 141  
QY 169 HMGFP-----LKG-----AKGISCHDCKNKE-----CEKLCF 195  
DB 142 QAGFYSEVSSAKATCLAQSNCKVGLRVVLKGDWNTLCAASCYDLKTRDGAELYHETLP 201  
QY 196 T 196

DB 202 T 202

Search completed: September 13, 2003, 07:05:34  
Job time : 42 secs